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LOGINID:ssspt189dxw

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

\* \* \* \* \* Welcome to STN International \* \* \* \* \*

NEWS	1		Web Page for STN Seminar Schedule - N. America
NEWS	2	JAN 02	STN pricing information for 2008 now available
NEWS	3	JAN 16	CAS patent coverage enhanced to include exemplified prophetic substances
NEWS	4	JAN 28	USPATFULL, USPAT2, and USPATOLD enhanced with new custom IPC display formats
NEWS	5	JAN 28	MARPAT searching enhanced
NEWS	6	JAN 28	USGENE now provides USPTO sequence data within 3 days of publication
NEWS	7	JAN 28	TOXCENTER enhanced with reloaded MEDLINE segment
NEWS	8	JAN 28	MEDLINE and LMEDLINE reloaded with enhancements
NEWS	9	FEB 08	STN Express, Version 8.3, now available
NEWS	10	FEB 20	PCI now available as a replacement to DPCI
NEWS	11	FEB 25	IFIREF reloaded with enhancements
NEWS	12	FEB 25	IMSPRODUCT reloaded with enhancements
NEWS	13	FEB 29	WPINDEX/WPIDS/WPIX enhanced with ECLA and current U.S. National Patent Classification
NEWS	14	MAR 31	IFICDB, IFIPAT, and IFIUIDB enhanced with new custom IPC display formats
NEWS	15	MAR 31	CAS REGISTRY enhanced with additional experimental spectra
NEWS	16	MAR 31	CA/CAPplus and CASREACT patent number format for U.S. applications updated
NEWS	17	MAR 31	LPCI now available as a replacement to LDPCI
NEWS	18	MAR 31	EMBASE, EMBAL, and LEMBASE reloaded with enhancements
NEWS	19	APR 04	STN AnaVist, Version 1, to be discontinued
NEWS	20	APR 15	WPIDS, WPINDEX, and WPIX enhanced with new predefined hit display formats
NEWS	21	APR 28	EMBASE Controlled Term thesaurus enhanced
NEWS	22	APR 28	IMSRESEARCH reloaded with enhancements
NEWS	23	MAY 30	INPAFAMDB now available on STN for patent family searching
NEWS	24	MAY 30	DGENE, PCTGEN, and USGENE enhanced with new homology sequence search option
NEWS	25	JUN 06	EPFULL enhanced with 260,000 English abstracts
NEWS	26	JUN 06	KOREAPAT updated with 41,000 documents
NEWS	27	JUN 13	USPATFULL and USPAT2 updated with 11-character patent numbers for U.S. applications
NEWS	28	JUN 19	CAS REGISTRY includes selected substances from web-based collections
NEWS	29	JUN 25	CA/CAPplus and USPAT databases updated with IPC reclassification data
NEWS	30	JUN 30	AEROSPACE enhanced with more than 1 million U.S. patent records
NEWS	31	JUN 30	EMBASE, EMBAL, and LEMBASE updated with additional options to display authors and affiliated

```

                                organizations
NEWS 32  JUN 30  STN on the Web enhanced with new STN AnaVist
                                Assistant and BLAST plug-in
NEWS 33  JUN 30  STN AnaVist enhanced with database content from EPFULL

NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,
                                AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.

NEWS HOURS      STN Operating Hours Plus Help Desk Availability
NEWS LOGIN      Welcome Banner and News Items
NEWS IPC8       For general information regarding STN implementation of IPC 8

```

Enter NEWS followed by the item number or name to see news on that specific topic.

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\* \* \* \* \* STN Columbus \* \* \* \* \*

FILE 'HOME' ENTERED AT 13:55:21 ON 07 JUL 2008

=> index bioscience

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
0.21	0.21

FULL ESTIMATED COST

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 13:55:47 ON 07 JUL 2008

69 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view search error messages that display as 0\* with SET DETAIL OFF.

=> s Lactobacillus reuteri and toxin(p)bind? and CD4+ cell? and (food or tablet or dietary supplement or confectionery or drug)  
0\* FILE ADISCTI

=> s Lactobacillus reuteri and toxin(p)bind? and CD4+ cells  
0\* FILE ADISCTI

=> s Lactobacillus reuteri and toxin(p)bind?

```

0* FILE ADISNEWS
0* FILE ANTE
0* FILE AQUALINE
0* FILE BIOENG
1* FILE BIOTECHABS
1* FILE BIOTECHDS
0* FILE BIOTECHNO
2 FILE CAPLUS
0* FILE CEABA-VTB
0* FILE CIN

```

27 FILES SEARCHED...

```

0* FILE ESBIOWASE
0* FILE FOMAD

```

0\* FILE FOREGE  
 2\* FILE FROSTI  
 0\* FILE FSTA  
 5 FILE GENBANK  
 1 FILE IFIPAT  
 0\* FILE KOSMET  
 0\* FILE NTIS  
 0\* FILE NUTRACEUT  
 1\* FILE PASCAL  
 0\* FILE PHARMAML  
 1 FILE SCISEARCH  
 1 FILE TOXCENTER  
 60 FILES SEARCHED...  
 21 FILE USPATFULL  
 3 FILE USPAT2  
 0\* FILE WATER  
 2 FILE WPIDS  
 2 FILE WPINDEX

13 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STNINDEX

L1 QUE LACTOBACILLUS REUTERI AND TOXIN(P) BIND?

=> file biotechds biotechabs caplus frosti genbank ifipat pascal scisearch  
 toxcenter uspatfull uspat2

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	3.90	4.11

FILE 'BIOTECHDS' ENTERED AT 13:59:37 ON 07 JUL 2008  
 COPYRIGHT (C) 2008 THOMSON REUTERS

FILE 'BIOTECHABS' ACCESS NOT AUTHORIZED

FILE 'CAPLUS' ENTERED AT 13:59:37 ON 07 JUL 2008  
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 PLEASE SEE "HELP USAGETERMS" FOR DETAILS.  
 COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'FROSTI' ENTERED AT 13:59:37 ON 07 JUL 2008  
 COPYRIGHT (C) 2008 Leatherhead Food Research Association

FILE 'GENBANK' ENTERED AT 13:59:37 ON 07 JUL 2008

FILE 'IFIPAT' ENTERED AT 13:59:37 ON 07 JUL 2008  
 COPYRIGHT (C) 2008 IFI CLAIMS(R) Patent Services (IFI)

FILE 'PASCAL' ENTERED AT 13:59:37 ON 07 JUL 2008  
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FILE 'SCISEARCH' ENTERED AT 13:59:37 ON 07 JUL 2008  
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FILE 'TOXCENTER' ENTERED AT 13:59:37 ON 07 JUL 2008  
 COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'USPATFULL' ENTERED AT 13:59:37 ON 07 JUL 2008  
 CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'USPAT2' ENTERED AT 13:59:37 ON 07 JUL 2008  
CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

```
=> s l1
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'TOXIN(P) BIND?'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'TOXIN(P) BIND?'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'TOXIN(P) BIND?'
L2          38 L1
```

```
=> rem dup l2
DUP IS NOT VALID HERE
The DELETE command is used to remove various items stored by the
system.
```

To delete a saved query, saved answer set, saved L-number list, SDI request, batch request, mailing list, or user-defined cluster, format, or search field, enter the name. The name may include ? for left, right, or simultaneous left and right truncation.

Examples:

```
DELETE BIO?/Q          - delete query names starting with BIO
DELETE ?DRUG/A          - delete answer set names ending with DRUG
DELETE ?ELEC?/L         - delete L-number lists containing ELEC
DELETE ANTICOAG/S       - delete SDI request
DELETE ENZYME/B         - delete batch request
DELETE .MYCLUSTER       - delete user-defined cluster
DELETE .MYFORMAT        - delete user-defined display format
DELETE .MYFIELD         - delete user-defined search field
DELETE NAMELIST MYLIST - delete mailing list
```

To delete an ordered document or an offline print, enter its number.

Examples:

```
DELETE P123001C        - delete print request
DELETE D134002C        - delete document order request
```

To delete an individual L-number or range of L-numbers, enter the L-number or L-number range. You may also enter DELETE LAST followed by a number, n, to delete the last n L-numbers. RENUMBER or NORENUMBER may also be explicitly specified to override the value of SET RENUMBER.

Examples:

```
DELETE L21              - delete a single L-number
DELETE L3-L6            - delete a range of L-numbers
DELETE LAST 4           - delete the last 4 L-numbers
DELETE L33-             - delete L33 and any higher L-number
DELETE -L55             - delete L55 and any lower L-number
DELETE L2-L6 RENUMBER   - delete a range of L-numbers and
                        renumber remaining L-numbers
DELETE RENUMBER         - renumber L-numbers after deletion of
                        intermediate L-numbers
```

Entire sets of saved items, SDI requests, batch requests, user-defined items, or E-numbers can be deleted.



Examples:

```
DELETE SAVED/Q - delete all saved queries
DELETE SAVED/A - delete all saved answer sets
DELETE SAVED/L - delete all saved L-number lists
DELETE SAVED - delete all saved queries, answer sets,
                and L-number lists
DELETE SAVED/S - delete all SDI requests
DELETE SAVED/B - delete all batch requests
DELETE CLUSTER - delete all user-defined clusters
DELETE FORMAT - delete all user-defined display formats
DELETE FIELD - delete all user-defined search fields
DELETE SELECT - delete all E-numbers
DELETE HISTORY - delete all L-numbers and restart the
                  session at L1
```

To delete an entire multifile SDI request, enter DELETE and the name of the request. To delete a component from the multifile SDI, enter DELETE and the name of the component.

```
=> dup rem l2
DUPLICATE IS NOT AVAILABLE IN 'GENBANK'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L2
L3          34 DUP REM L2 (4 DUPLICATES REMOVED)
```

```
=> s l3 and (tablet or food or dietary supplement or confectionery or drug) and
product
L4          27 L3 AND (TABLET OR FOOD OR DIETARY SUPPLEMENT OR CONFECTIONERY
                OR DRUG) AND PRODUCT
```

```
=> rem dup l4
DUP IS NOT VALID HERE
The DELETE command is used to remove various items stored by the
system.
```

To delete a saved query, saved answer set, saved L-number list, SDI request, batch request, mailing list, or user-defined cluster, format, or search field, enter the name. The name may include ? for left, right, or simultaneous left and right truncation.

Examples:

```
DELETE BIO?/Q - delete query names starting with BIO
DELETE ?DRUG/A - delete answer set names ending with DRUG
DELETE ?ELEC?/L - delete L-number lists containing ELEC
DELETE ANTICOAG/S - delete SDI request
DELETE ENZYME/B - delete batch request
DELETE .MYCLUSTER - delete user-defined cluster
DELETE .MYFORMAT - delete user-defined display format
DELETE .MYFIELD - delete user-defined search field
DELETE NAMELIST MYLIST - delete mailing list
```

To delete an ordered document or an offline print, enter its number.

Examples:

```
DELETE P123001C - delete print request
DELETE D134002C - delete document order request
```

To delete an individual L-number or range of L-numbers, enter the L-number or L-number range. You may also enter DELETE LAST followed by a number, n, to delete the last n L-numbers. RENUMBER or NORENUMBER may also be explicitly specified to override the value of SET RENUMBER.

Examples:

```
DELETE L21           - delete a single L-number
DELETE L3-L6         - delete a range of L-numbers
DELETE LAST 4        - delete the last 4 L-numbers
DELETE L33-          - delete L33 and any higher L-number
DELETE -L55          - delete L55 and any lower L-number
DELETE L2-L6 RENUMBER - delete a range of L-numbers and
                      renumber remaining L-numbers
DELETE RENUMBER      - renumber L-numbers after deletion of
                      intermediate L-numbers
```

Entire sets of saved items, SDI requests, batch requests, user-defined items, or E-numbers can be deleted.

Examples:

```
DELETE SAVED/Q - delete all saved queries
DELETE SAVED/A - delete all saved answer sets
DELETE SAVED/L - delete all saved L-number lists
DELETE SAVED   - delete all saved queries, answer sets,
                and L-number lists
DELETE SAVED/S - delete all SDI requests
DELETE SAVED/B - delete all batch requests
DELETE CLUSTER - delete all user-defined clusters
DELETE FORMAT  - delete all user-defined display formats
DELETE FIELD   - delete all user-defined search fields
DELETE SELECT  - delete all E-numbers
DELETE HISTORY - delete all L-numbers and restart the
                session at L1
```

To delete an entire multifile SDI request, enter DELETE and the name of the request. To delete a component from the multifile SDI, enter DELETE and the name of the component.

```
=> dup rem l4
DUPLICATE IS NOT AVAILABLE IN 'GENBANK'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L4
L5          27 DUP REM L4 (0 DUPLICATES REMOVED)
```

```
=> d 15 1-27
```

```
L5  ANSWER 1 OF 27  USPATFULL on STN
AN   2007:296111  USPATFULL
TI   Lactobacillus acidophillus nucleic acid sequences encoding cell surface
      protein homologues and uses therefore
IN   Klaenhammer, Todd R., Raleigh, NC, UNITED STATES
      Altermann, Eric, Palmerston North, NEW ZEALAND
      Buck, B. Logan, Banner Elk, NC, UNITED STATES
      Russell, W. Michael, Newburgh, IN, UNITED STATES
PA   North Carolina State University, Raleigh, NC, UNITED STATES (U.S.
      corporation)
PI   US 20070258955      A1  20071108
AI   US 2007-701335      A1  20070201 (11)
RLI  Division of Ser. No. US 2004-831070, filed on 23 Apr 2004, PENDING
```

PRAI US 2003-465621P 20030425 (60)  
 DT Utility  
 FS APPLICATION  
 LN.CNT 5104  
 INCL INCLM: 424/093.400  
 INCLS: 435/252.100; 435/252.900; 435/320.100; 435/006.000; 435/007.100;  
 435/070.100; 514/002.000; 530/300.000; 530/387.100; 536/023.100  
 NCL NCLM: 424/093.400  
 NCLS: 435/006.000; 435/007.100; 435/070.100; 435/252.100; 435/252.900;  
 435/320.100; 514/002.000; 530/300.000; 530/387.100; 536/023.100  
 IC IPCI A61K0035-00 [I,A]; A61K0038-00 [I,A]; A61P0001-00 [I,A];  
 C07H0021-02 [I,A]; C07H0021-00 [I,C\*]; C07K0016-00 [I,A];  
 C07K0004-00 [I,A]; C12N0001-20 [I,A]; C12N0015-00 [I,A];  
 C12P0021-04 [I,A]; C12Q0001-68 [I,A]  
 IPCR A61K0035-00 [I,C]; A61K0035-00 [I,A]; A61K0038-00 [I,C];  
 A61K0038-00 [I,A]; A61P0001-00 [I,C]; A61P0001-00 [I,A];  
 C07H0021-00 [I,C]; C07H0021-02 [I,A]; C07H0021-04 [I,A];  
 C07K0004-00 [I,C]; C07K0004-00 [I,A]; C07K0014-195 [I,C\*];  
 C07K0014-335 [I,A]; C07K0016-00 [I,C]; C07K0016-00 [I,A];  
 C12N0001-20 [I,C]; C12N0001-20 [I,A]; C12N0001-21 [I,C\*];  
 C12N0001-21 [I,A]; C12N0009-00 [I,C\*]; C12N0009-00 [I,A];  
 C12N0015-00 [I,C]; C12N0015-00 [I,A]; C12P0021-04 [I,C];  
 C12P0021-04 [I,A]; C12P0021-06 [I,C\*]; C12P0021-06 [I,A];  
 C12Q0001-68 [I,C]; C12Q0001-68 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 2 OF 27 USPATFULL on STN  
 AN 2007:197155 USPATFULL  
 TI Lactobacillus acidophilus nucleic acid sequences encoding cell surface  
 protein homologues and uses therefore  
 IN Klaenhammer, Todd R., Raleigh, NC, UNITED STATES  
 Altermann, Eric, Palmerston North, NEW ZEALAND  
 Buck, B. Logan, Banner Elk, NC, UNITED STATES  
 Russell, W. Michael, Newburgh, IN, UNITED STATES  
 PA North Carolina State University, Raleigh, NC, UNITED STATES, 27695-8210  
 (U.S. corporation)  
 PI US 20070172495 A1 20070726  
 AI US 2007-701319 A1 20070201 (11)  
 RLI Division of Ser. No. US 2004-831070, filed on 23 Apr 2004, PENDING  
 PRAI US 2003-465621P 20030425 (60)  
 DT Utility  
 FS APPLICATION  
 LN.CNT 5104  
 INCL INCLM: 424/234.100  
 INCLS: 514/044.000; 435/006.000; 435/007.320; 435/069.100; 435/252.900;  
 435/471.000; 530/350.000; 536/023.700  
 NCL NCLM: 424/234.100  
 NCLS: 435/006.000; 435/007.320; 435/069.100; 435/252.900; 435/471.000;  
 514/044.000; 530/350.000; 536/023.700  
 IC IPCI A61K0048-00 [I,A]; A61K0039-02 [I,A]; C12Q0001-68 [I,A];  
 G01N0033-554 [I,A]; C07H0021-04 [I,A]; C07H0021-00 [I,C\*];  
 C12P0021-06 [I,A]; C07K0014-335 [I,A]; C07K0014-195 [I,C\*]  
 IPCR A61K0048-00 [I,C]; A61K0048-00 [I,A]; A61K0039-02 [I,C];  
 A61K0039-02 [I,A]; C07H0021-00 [I,C]; C07H0021-04 [I,A];  
 C07K0014-195 [I,C]; C07K0014-335 [I,A]; C12N0001-21 [I,C\*];  
 C12N0001-21 [I,A]; C12N0009-00 [I,C\*]; C12N0009-00 [I,A];  
 C12P0021-06 [I,C]; C12P0021-06 [I,A]; C12Q0001-68 [I,C];  
 C12Q0001-68 [I,A]; G01N0033-554 [I,C]; G01N0033-554 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 3 OF 27 USPATFULL on STN  
 AN 2007:140436 USPATFULL

TI Delivery of trefoil peptides  
 IN Hans, Wolfgang Christian, Landshut, GERMANY, FEDERAL REPUBLIC OF  
 Steidler, Lothar, Lokeren, BELGIUM  
 Remaut, Erik Rene, Lovendegem, BELGIUM  
 PI US 20070122427 A1 20070531  
 AI US 2007-654879 A1 20070118 (11)  
 RLI Division of Ser. No. US 2002-30390, filed on 16 Apr 2002, PENDING A 371  
 of International Ser. No. WO 2000-EP6343, filed on 5 Jul 2000  
 PRAI EP 1999-870143 19990705  
 DT Utility  
 FS APPLICATION  
 LN.CNT 1335  
 INCL INCLM: 424/200.100  
 INCLS: 435/252.300; 435/252.900  
 NCL NCLM: 424/200.100  
 NCLS: 435/252.300; 435/252.900  
 IC IPCI A61K0039-02 [I,A]; C12N0001-21 [I,A]  
 IPCR A61K0039-02 [I,C]; A61K0039-02 [I,A]; C12N0001-21 [I,C];  
 C12N0001-21 [I,A]  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 4 OF 27 USPATFULL on STN  
 AN 2007:134502 USPATFULL  
 TI Corynebacterium glutamicum genes encoding metabolic pathway proteins  
 IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF  
 Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF  
 Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF  
 Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF  
 Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF  
 PA BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF  
 (non-U.S. corporation)  
 PI US 20070117183 A1 20070524  
 AI US 2006-511140 A1 20060828 (11)  
 RLI Division of Ser. No. US 2005-55822, filed on 11 Feb 2005, PENDING  
 Continuation of Ser. No. US 2000-606740, filed on 23 Jun 2000, ABANDONED  
 PRAI DE 1999-19932125 19990709  
 DE 1999-19932227 19990709  
 DE 1999-19932228 19990709  
 DE 1999-19932230 19990709  
 DE 1999-19933005 19990714  
 DE 1999-19933006 19990714  
 DE 1999-19940764 19990827  
 DE 1999-19940766 19990827  
 DE 1999-19940832 19990827  
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 DE 1999-19942077 19990903  
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 DE 1999-19932126 19990709  
 DE 1999-19932229 19990709  
 DE 1999-19941396 19990831  
 DE 1999-19942087 19990903  
 DE 1999-19930476 19990701  
 DE 1999-19931419 19990708  
 DE 1999-19931420 19990708  
 DE 1999-19932206 19990709  
 DE 1999-19942088 19990903  
 DE 1999-19942124 19990903  
 DE 1999-19932928 19990714  
 DE 1999-19931415 19990708  
 DE 1999-19931424 19990708

DE	1999-19931428	19990708
DE	1999-19931434	19990708
DE	1999-19931435	19990708
DE	1999-19931443	19990708
DE	1999-19931453	19990708
DE	1999-19931457	19990708
DE	1999-19931465	19990708
DE	1999-19931478	19990708
DE	1999-19931510	19990708
DE	1999-19931541	19990708
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DE	1999-19931592	19990708
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DE	1999-19931634	19990708
DE	1999-19931636	19990708
DE	1999-19932130	19990709
DE	1999-19932186	19990709
DE	1999-19932922	19990714
DE	1999-19932926	19990714
DE	1999-19933004	19990714
DE	1999-19940765	19990827
DE	1999-19941380	19990831
DE	1999-19941394	19990831
DE	1999-19942076	19990903
DE	1999-19942086	19990903
DE	1999-19942095	19990903
DE	1999-19942129	19990903
US	1999-141031P	19990625 (60)
US	1999-142101P	19990702 (60)
US	1999-148613P	19990812 (60)
US	2000-187970P	20000309 (60)

DT Utility  
FS APPLICATION

LN.CNT 8386

INCL INCL: 435/069.100  
INCLS: 435/106.000; 435/115.000; 435/193.000; 435/252.300; 435/471.000;  
536/023.200

NCL NCLM: 435/069.100  
NCLS: 435/106.000; 435/115.000; 435/193.000; 435/252.300; 435/471.000;  
536/023.200

IC IPCI C07H0021-04 [I,A]; C07H0021-00 [I,C\*]; C12P0021-06 [I,A];  
C12P0013-04 [I,A]; C12P0013-08 [I,A]; C12P0013-00 [I,C\*];  
C12N0009-10 [I,A]; C12N0015-74 [I,A]; C12N0001-21 [I,A]  
IPCR C07H0021-00 [I,C]; C07H0021-04 [I,A]; C12N0001-21 [I,C];  
C12N0001-21 [I,A]; C12N0009-10 [I,C]; C12N0009-10 [I,A];  
C12N0015-74 [I,C]; C12N0015-74 [I,A]; C12P0013-00 [I,C];  
C12P0013-04 [I,A]; C12P0013-08 [I,A]; C12P0021-06 [I,C];  
C12P0021-06 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 5 OF 27 USPATFULL on STN

AN 2007:127377 USPATFULL

TI Delivery of trefoil peptides

IN Hans, Wolfgang Christian, Landshut, GERMANY, FEDERAL REPUBLIC OF  
Steidler, Lothar, Lokeren, BELGIUM  
Remaut, Erik Rene, Lovendegem, BELGIUM

PI US 20070110723 A1 20070517

AI US 2007-654985 A1 20070118 (11)

RLI Continuation of Ser. No. US 2002-30390, filed on 16 Apr 2002, PENDING A  
371 of International Ser. No. WO 2000-EP6343, filed on 5 Jul 2000

PRAI EP 1999-870143 19990705

DT Utility

FS APPLICATION  
LN.CNT 1328  
INCL INCLM: 424/093.200  
INCLS: 424/093.450  
NCL NCLM: 424/093.200  
NCLS: 424/093.450  
IC IPCI A61K0048-00 [I,A]  
IPCR A61K0048-00 [I,C]; A61K0048-00 [I,A]; C12N0015-09 [I,C\*];  
C12N0015-09 [I,A]; A61K0035-66 [I,C\*]; A61K0035-74 [I,A];  
A61K0038-00 [I,C\*]; A61K0038-00 [I,A]; A61P0001-00 [I,C\*];  
A61P0001-04 [I,A]; C07K0014-435 [I,C\*]; C07K0014-575 [I,A];  
C12N0001-21 [I,C\*]; C12N0001-21 [I,A]; C12N0015-16 [I,C\*];  
C12N0015-16 [I,A]; C12N0015-74 [I,C\*]; C12N0015-74 [I,A];  
C12R0001-01 [N,A]  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 6 OF 27 USPATFULL on STN  
AN 2007:130427 USPATFULL  
TI Delivery of trefoil peptides  
IN Hans, Wolfgang Christian, Landshut, GERMANY, FEDERAL REPUBLIC OF  
Steidler, Lothar, Lokeren, BELGIUM  
Remaut, Erik Rene, Lonendegem, BELGIUM  
PA Vlaams Interuniversitair Instituut voor Biotechnologie, BELGIUM  
(non-U.S. corporation)  
PI US 7220418 B1 20070522  
WO 2001002570 20010111  
AI US 2000-30390 20000705 (10)  
WO 2000-EP6343 20000705  
20020416 PCT 371 date  
PRAI EP 1999-870143 19990705  
DT Utility  
FS GRANTED  
LN.CNT 1334  
INCL INCLM: 424/200.100  
INCLS: 424/093.450; 424/093.200; 424/234.100; 424/192.100; 514/925.000  
NCL NCLM: 424/200.100  
NCLS: 424/093.200; 424/093.450; 424/192.100; 424/234.100; 514/925.000  
IC IPCI A01N0063-00 [I,A]; A61K0039-02 [I,A]; A61K0039-00 [I,A]  
IPCR A01N0063-00 [I,C]; A01N0063-00 [I,A]; C12N0015-09 [I,C\*];  
C12N0015-09 [I,A]; A61K0035-66 [I,C\*]; A61K0035-74 [I,A];  
A61K0038-00 [I,C\*]; A61K0038-00 [I,A]; A61K0039-00 [I,C];  
A61K0039-00 [I,A]; A61K0039-02 [I,C]; A61K0039-02 [I,A];  
A61K0048-00 [I,C\*]; A61K0048-00 [I,A]; A61P0001-00 [I,C\*];  
A61P0001-04 [I,A]; C07K0014-435 [I,C\*]; C07K0014-575 [I,A];  
C12N0001-21 [I,C\*]; C12N0001-21 [I,A]; C12N0015-16 [I,C\*];  
C12N0015-16 [I,A]; C12N0015-74 [I,C\*]; C12N0015-74 [I,A];  
C12R0001-01 [N,A]  
EXF 424/200.1; 424/192.1; 424/184.1; 424/234.1; 424/244.1; 424/246.1;  
424/93.2; 424/93.45; 514/2; 514/925; 435/69.3; 435/69.1; 435/71.1;  
435/252.9  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 7 OF 27 IFIPAT COPYRIGHT 2008 IFI on STN  
AN 11053905 IFIPAT;IFIUDB;IFICDB  
TI METHOD OF IMPROVING IMMUNE FUNCTION IN MAMALS USING LACTOBACILLUS  
REUTERI STRAINS  
IN Kang Ho-Jin (KR); Kwon Ik-boo (KR); Lee Dong-Seog (KR); Mollstam Bo (SE)  
PA Unassigned Or Assigned To Individual (68000)  
PI US 2006002907 A1 20060105  
AI US 2002-531651 20021018  
WO 2002-SE1903 20021018  
20050415 PCT 371 date

20050415 PCT 102(e) date  
FI US 2006002907 20060105  
DT Utility; Patent Application - First Publication  
FS CHEMICAL  
APPLICATION  
ED Entered STN: 9 Jan 2006  
Last Updated on STN: 9 Jan 2006  
CLMN 9  
GI 1 Figure(s).  
FIG. 1. Confirmation of inhibitory ability against the binding of vero  
cytotoxin(VT) and Gb3 receptor in a culture supernatant of L. reuteri  
through competitive ELISA. Each reacted as follows, on plates coated with  
Gb3, followed by performing ELISA using mAb against VT.

L5 ANSWER 8 OF 27 USPATFULL on STN  
AN 2006:274450 USPATFULL  
TI Gene products differentially expressed in cancerous cells  
IN Scott, Elizabeth M., Emeryville, CA, UNITED STATES  
Lamson, George, Emeryville, CA, UNITED STATES  
Kassam, Altaf, Emeryville, CA, UNITED STATES  
Zhang, Guozhong, Emeryville, CA, UNITED STATES  
Sakamoto, Doreen, Emeryville, CA, UNITED STATES  
Garcia, Pablo Dominguez, Emeryville, CA, UNITED STATES  
May, Theresa, Emeryville, CA, UNITED STATES  
Kennedy, Giulia C., Emeryville, CA, UNITED STATES  
Kang, Sanmao, Emeryville, CA, UNITED STATES  
Reinhard, Christoph, Emeryville, CA, UNITED STATES  
Jefferson, Ann Bennett, Emeryville, CA, UNITED STATES  
PA Chiron Corporation (U.S. corporation)  
PI US 20060234246 A1 20061019  
AI US 2004-934842 A1 20040902 (10)  
RLI Continuation-in-part of Ser. No. US 2002-165835, filed on 6 Jun 2002,  
ABANDONED Continuation of Ser. No. US 2000-490818, filed on 25 Jan 2000,  
GRANTED, Pat. No. US 6429302 Continuation-in-part of Ser. No. US  
2001-883152, filed on 15 Jun 2001, ABANDONED Continuation-in-part of  
Ser. No. WO 2003-US15465, filed on 16 May 2003, PENDING  
PRAI US 1999-118302P 19990202 (60)  
US 2000-211835P 20000615 (60)  
US 2003-445222P 20030204 (60)  
US 2002-381533P 20020517 (60)  
DT Utility  
FS APPLICATION  
LN.CNT 17024  
INCL INCLM: 435/006.000  
INCLS: 435/007.230; 435/069.100; 435/320.100; 435/325.000; 530/350.000;  
530/388.800; 536/023.500  
NCL NCLM: 435/006.000  
NCLS: 435/007.230; 435/069.100; 435/320.100; 435/325.000; 530/350.000;  
530/388.800; 536/023.500  
IC IPCI C12Q0001-68 [I,A]; G01N0033-574 [I,A]; C07H0021-04 [I,A];  
C07H0021-00 [I,C\*]; C12P0021-06 [I,A]; C07K0014-82 [I,A];  
C07K0016-30 [I,A]; C07K0016-18 [I,C\*]  
IPCR C12Q0001-68 [I,C]; C12Q0001-68 [I,A]; C07H0021-00 [I,C];  
C07H0021-04 [I,A]; C07K0014-82 [I,C]; C07K0014-82 [I,A];  
C07K0016-18 [I,C]; C07K0016-30 [I,A]; C12P0021-06 [I,C];  
C12P0021-06 [I,A]; G01N0033-574 [I,C]; G01N0033-574 [I,A]  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 9 OF 27 USPATFULL on STN  
AN 2006:98984 USPATFULL  
TI Corynebacterium glutamicum genes encoding metabolic pathway proteins  
IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF

Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF  
 Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF  
 Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF  
 Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF  
 PA BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF  
 (non-U.S. corporation)  
 PI US 20060084152 A1 20060420  
 AI US 2005-239674 A1 20050928 (11)  
 RLI Continuation of Ser. No. US 2000-746660, filed on 22 Dec 2000, ABANDONED  
 Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,  
 ABANDONED Continuation-in-part of Ser. No. US 2000-603124, filed on 23  
 Jun 2000, ABANDONED  
 PRAI DE 1999-19932125 19990709  
 DE 1999-19932227 19990709  
 DE 1999-19932228 19990709  
 DE 1999-19932230 19990709  
 DE 1999-19933005 19990714  
 DE 1999-19933006 19990714  
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 DE 1999-19932922 19990714  
 DE 1999-19932926 19990714  
 DE 1999-19933004 19990714  
 DE 1999-19940765 19990827  
 DE 1999-19941380 19990831  
 DE 1999-19941394 19990831



DE 1999-19942076 19990903  
 DE 1999-19942086 19990903  
 DE 1999-19942095 19990903  
 DE 1999-19942129 19990903  
 DE 1999-19932124 19990709  
 DE 1999-19932127 19990709  
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 DE 1999-19932208 19990709  
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 DE 1999-19932914 19990709  
 DE 1999-19940768 19990827  
 DE 1999-19940831 19990827  
 DE 1999-19941385 19990831  
 US 1999-141031P 19990625 (60)  
 US 1999-142101P 19990702 (60)  
 US 1999-148613P 19990812 (60)  
 US 2000-187970P 20000309 (60)  
 US 1999-141031P 19990625 (60)  
 US 1999-143694P 19990714 (60)  
 US 1999-151778P 19990831 (60)  
 DT Utility  
 FS APPLICATION  
 LN.CNT 14822  
 INCL INCLM: 435/113.000  
 INCLS: 435/115.000; 435/252.300  
 NCL NCLM: 435/113.000  
 NCLS: 435/115.000; 435/252.300  
 IC IPCI C12P0013-12 [I,A]; C12P0013-08 [I,A]; C12P0013-00 [I,C\*];  
 C12N0001-20 [I,A]  
 IPCR C12P0013-00 [I,C]; C12P0013-12 [I,A]; C12N0001-20 [I,C];  
 C12N0001-20 [I,A]; C12P0013-08 [I,A]  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.  
  
 L5 ANSWER 10 OF 27 USPATFULL on STN  
 AN 2006:211028 USPATFULL  
 TI Nucleic acid sequences relating to Bacteroides fragilis for diagnostics  
 and therapeutics  
 IN Breton, Gary L., Marlboro, MA, UNITED STATES  
 PA Oscient Pharmaceuticals Corporation, Waltham, MA, UNITED STATES (U.S.  
 corporation)  
 PI US 7090973 B1 20060815  
 AI US 2000-540209 20000404 (9)  
 PRAI US 1999-128705P 19990409 (60)  
 DT Utility  
 FS GRANTED  
 LN.CNT 38850  
 INCL INCLM: 435/006.000  
 INCLS: 435/091.200; 536/023.500; 536/024.310; 536/024.330  
 NCL NCLM: 435/006.000  
 NCLS: 435/091.200; 536/023.500; 536/024.310; 536/024.330  
 IC IPCI C12Q0001-68 [I,A]; C12P0019-34 [I,A]; C12P0019-00 [I,C\*];  
 C07H0021-02 [I,A]; C07H0021-04 [I,A]; C07H0021-00 [I,C\*]  
 EXF 435/91.1; 435/91.2; 435/6; 435/320.1; 435/325; 435/352.3; 536/23.1;  
 536/24.1; 536/23.7; 536/24.32; 536/24.3; 514/44  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.  
  
 L5 ANSWER 11 OF 27 USPATFULL on STN  
 AN 2006:146715 USPATFULL  
 TI Nucleic acid and amino acid sequences relating to Staphylococcus  
 epidermidis for diagnostics and therapeutics  
 IN Doucette-Stamm, Lynn, Framingham, MA, UNITED STATES

Bush, David, Somerville, MA, UNITED STATES  
 PA Wyeth, Madison, NJ, UNITED STATES (U.S. corporation)  
 PI US 7060458 B1 20060613  
 AI US 1999-450969 19991129 (9)  
 RLI Continuation-in-part of Ser. No. US 1998-134001, filed on 13 Aug 1998,  
 Pat. No. US 6380370, issued on 30 Apr 2002  
 PRAI US 1997-64964P 19971108 (60)  
 US 1997-55779P 19970814 (60)  
 DT Utility  
 FS GRANTED  
 LN.CNT 35708  
 INCL INCLM: 435/069.100  
 INCLS: 435/252.300; 435/320.100; 435/325.000; 536/023.700; 536/024.320  
 NCL NCLM: 435/069.100  
 NCLS: 435/252.300; 435/320.100; 435/325.000; 536/023.700; 536/024.320  
 IC IPCI C07H0021-04 [I,A]; C07H0021-00 [I,C\*]  
 IPCR C07H0021-00 [I,C]; C07H0021-04 [I,A]; C12N0001-21 [I,C\*];  
 C12N0001-21 [I,A]; C12Q0001-68 [I,C\*]; C12Q0001-68 [I,A]  
 EXF 435/6; 435/91.2; 435/69.1; 536/22.1; 536/23.1; 536/24.3  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 12 OF 27 USPATFULL on STN  
 AN 2005:299042 USPATFULL  
 TI Corynebacterium glutamicum genes encoding metabolic pathway proteins  
 IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF  
 Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF  
 Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF  
 Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF  
 Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF  
 PA BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF  
 (non-U.S. corporation)  
 PI US 20050260707 A1 20051124  
 AI US 2005-55822 A1 20050211 (11)  
 RLI Continuation of Ser. No. US 2000-606740, filed on 23 Jun 2000, ABANDONED  
 PRAI DE 1999-19932125 19990709  
 DE 1999-19932227 19990709  
 DE 1999-19932228 19990709  
 DE 1999-19932230 19990709  
 DE 1999-19933005 19990714  
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 DE 1999-19932206 19990709  
 DE 1999-19942088 19990903  
 DE 1999-19942124 19990903  
 DE 1999-19932928 19990714  
 DE 1999-19931415 19990708  
 DE 1999-19931424 19990708  
 DE 1999-19931428 19990708

DE	1999-19931434	19990708
DE	1999-19931435	19990708
DE	1999-19931443	19990708
DE	1999-19931453	19990708
DE	1999-19931457	19990708
DE	1999-19931465	19990708
DE	1999-19931478	19990708
DE	1999-19931510	19990708
DE	1999-109931541	19990708
DE	1999-19931573	19990708
DE	1999-19931592	19990708
DE	1999-19931632	19990708
DE	1999-19931634	19990708
DE	1999-19931636	19990708
DE	1999-19932130	19990708
DE	1999-19932186	19990709
DE	1999-19932922	19990714
DE	1999-19932926	19990714
DE	1999-19933004	19990714
DE	1999-19940765	19990827
DE	1999-19941380	19990831
DE	1999-19941394	19990831
DE	1999-19942076	19990903
DE	1999-19942086	19990903
DE	1999-19942095	19990903
DE	1999-19942129	19990903
US	1999-141031P	19990625 (60)
US	1999-142101P	19990702 (60)
US	1999-148613P	19990812 (60)
US	2000-187970P	20000309 (60)

DT Utility

FS APPLICATION

LN.CNT 8777

INCL INCLM: 435/069.100

INCLS: 435/106.000; 435/193.000; 435/252.300; 435/471.000; 536/023.200

NCL NCLM: 435/069.100

NCLS: 435/106.000; 435/193.000; 435/252.300; 435/471.000; 536/023.200

IC [7]

ICM C12P021-06

ICS C12P013-04; C07H021-04; C12N001-20; C12N015-74; C12N009-10

IPCI C12P0021-06 [ICM,7]; C12P0013-04 [ICS,7]; C12P0013-00 [ICS,7,C\*];  
C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C\*]; C12N0001-20 [ICS,7];  
C12N0015-74 [ICS,7]; C12N0009-10 [ICS,7]

IPCR C07H0021-00 [I,C\*]; C07H0021-04 [I,A]; C07K0014-195 [I,C\*];  
C07K0014-34 [I,A]; C12N0001-20 [I,C\*]; C12N0001-20 [I,A];  
C12N0009-00 [I,C\*]; C12N0009-00 [I,A]; C12N0009-10 [I,C\*];  
C12N0009-10 [I,A]; C12N0015-74 [I,C\*]; C12N0015-74 [I,A];  
C12P0013-00 [I,C\*]; C12P0013-04 [I,A]; C12P0021-06 [I,C\*];  
C12P0021-06 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 13 OF 27 USPATFULL on STN

AN 2005:268092 USPATFULL

TI Modified bacterial surface layer proteins

IN Pouwels, Pieter Hendrik, Rijswijk, NETHERLANDS

Smit, Egbert, Sittard, NETHERLANDS

Tielen, Frans, Prinsenbeek, NETHERLANDS

PI US 20050233408 A1 20051020

AI US 2003-500307 A1 20021223 (10)

WO 2002-EP14749 20021223

20041122 PCT 371 date

PRAI EP 2001-310937 20011228

DT Utility  
 FS APPLICATION  
 LN.CNT 2664  
 INCL INCLM: 435/034.000  
 INCLS: 530/395.000; 435/252.300  
 NCL NCLM: 435/034.000  
 NCLS: 435/252.300; 530/395.000  
 IC [7]  
 ICM C12Q001-04  
 ICS C12N001-21; C07K014-335  
 IPCI C12Q0001-04 [ICM,7]; C12N0001-21 [ICS,7]; C07K0014-335 [ICS,7];  
 C07K0014-195 [ICS,7,C\*]  
 IPCR C12N0015-09 [I,C\*]; C12N0015-09 [I,A]; A61K0039-02 [I,C\*];  
 A61K0039-02 [I,A]; A61P0031-00 [I,C\*]; A61P0031-04 [I,A];  
 C07K0014-195 [I,C\*]; C07K0014-335 [I,A]; C12N0001-15 [I,C\*];  
 C12N0001-15 [I,A]; C12N0001-19 [I,C\*]; C12N0001-19 [I,A];  
 C12N0001-20 [I,C\*]; C12N0001-20 [I,A]; C12N0001-21 [I,C\*];  
 C12N0001-21 [I,A]; C12N0005-10 [I,C\*]; C12N0005-10 [I,A];  
 C12N0015-31 [I,C\*]; C12N0015-31 [I,A]  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 14 OF 27 USPATFULL on STN  
 AN 2005:220997 USPATFULL  
 TI Corynebacterium glutamicum genes encoding proteins involved in  
 homeostasis and adaptation  
 IN Pompejus, Markus, Waldsee, GERMANY, FEDERAL REPUBLIC OF  
 Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF  
 Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF  
 Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF  
 PA Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF  
 BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF,  
 D-67056 (non-U.S. corporation)  
 PI US 20050191732 A1 20050901  
 AI US 2003-721922 A1 20031124 (10)  
 RLI Continuation of Ser. No. US 2000-603124, filed on 23 Jun 2000, ABANDONED  
 PRAI DE 1999-19931418 19990708  
 DE 1999-19932124 19990709  
 DE 1999-19932126 19990709  
 DE 1999-19932127 19990709  
 DE 1999-19932133 19990709  
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 DE 1999-19940765 19990827  
 DE 1999-19940768 19990827  
 DE 1999-19940831 19990827  
 DE 1999-19940832 19990827  
 DE 1999-19941385 19990831  
 DE 1999-19941396 19990831  
 DE 1999-19942087 19990903  
 US 1999-141031P 19990625 (60)  
 US 1999-143694P 19990714 (60)  
 US 1999-151778P 19990831 (60)  
 DT Utility  
 FS APPLICATION  
 LN.CNT 6552  
 INCL INCLM: 435/106.000  
 INCLS: 435/006.000; 435/069.100; 435/193.000; 435/252.300; 435/320.100;  
 536/023.200

NCL NCLM: 435/106.000  
 NCLS: 435/006.000; 435/069.100; 435/193.000; 435/252.300; 435/320.100;  
 536/023.200

IC [7]  
 ICM C12Q001-68  
 ICS C07H021-04; C12P013-04; C12N009-10; C12N001-21; C12N015-74  
 IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C\*];  
 C12P0013-04 [ICS,7]; C12P0013-00 [ICS,7,C\*]; C12N0009-10 [ICS,7];  
 C12N0001-21 [ICS,7]; C12N0015-74 [ICS,7]  
 IPCR C07H0021-00 [I,C\*]; C07H0021-04 [I,A]; C07K0014-195 [I,C\*];  
 C07K0014-34 [I,A]; C12N0001-21 [I,C\*]; C12N0001-21 [I,A];  
 C12N0009-00 [I,C\*]; C12N0009-00 [I,A]; C12N0009-10 [I,C\*];  
 C12N0009-10 [I,A]; C12N0015-74 [I,C\*]; C12N0015-74 [I,A];  
 C12P0001-04 [I,C\*]; C12P0001-04 [I,A]; C12P0013-00 [I,C\*];  
 C12P0013-04 [I,A]; C12Q0001-68 [I,C\*]; C12Q0001-68 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 15 OF 27 USPATFULL on STN  
 AN 2005:158196 USPATFULL  
 TI Nucleic acid and amino acid sequences relating to streptococcus  
 pneumoniae for diagnostics and therapeutics  
 IN Doucette-Stamm, Lynn A., Framingham, MA, UNITED STATES  
 Bush, David, Somerville, MA, UNITED STATES  
 PI US 20050136404 A1 20050623  
 AI US 2003-617320 A1 20030710 (10)  
 RLI Division of Ser. No. US 1998-107433, filed on 30 Jun 1998, PENDING  
 PRAI US 1997-51553P 19970702 (60)  
 US 1998-85131P 19980512 (60)  
 DT Utility  
 FS APPLICATION  
 LN.CNT 12957  
 INCL INCLM: 435/006.000  
 INCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.700  
 NCL NCLM: 435/006.000  
 NCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.700  
 IC [7]  
 ICM C12Q001-68  
 ICS C07H021-04; C12N001-21; C07K014-315  
 IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C\*];  
 C12N0001-21 [ICS,7]; C07K0014-315 [ICS,7]; C07K0014-195  
 [ICS,7,C\*]  
 IPCR C07H0021-00 [I,C\*]; C07H0021-02 [I,A]; C07H0021-04 [I,A];  
 C07K0014-195 [I,C\*]; C07K0014-315 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 16 OF 27 USPATFULL on STN  
 AN 2005:131152 USPATFULL  
 TI Lactobacillus acidophilus nucleic acid sequences encoding cell surface  
 protein homologues and uses therefore  
 IN Klaenhammer, Todd R., Raleigh, NC, UNITED STATES  
 Alterman, Eric, Apex, NC, UNITED STATES  
 Buck, B. Logan, Banner Elk, NC, UNITED STATES  
 Russell, W. Michael, Newburg, IN, UNITED STATES  
 PI US 20050112612 A1 20050526  
 US 7348420 B2 20080325  
 AI US 2004-831070 A1 20040423 (10)  
 PRAI US 2003-465621P 20030425 (60)  
 DT Utility  
 FS APPLICATION  
 LN.CNT 6100  
 INCL INCLM: 435/006.000  
 INCLS: 435/069.100; 435/183.000; 435/252.300; 435/320.100; 530/350.000;

536/023.200  
NCL NCLM: 536/023.100; 435/006.000  
NCLS: 435/069.100; 435/252.300; 435/320.100; 435/183.000; 530/350.000;  
536/023.200  
IC [7]  
ICM C12Q001-68  
ICS C07H021-04; C12P021-06; C12N009-00; C12N001-21; C07K014-335  
IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C\*];  
C12P0021-06 [ICS,7]; C12N0009-00 [ICS,7]; C12N0001-21 [ICS,7];  
C07K0014-335 [ICS,7]; C07K0014-195 [ICS,7,C\*]  
IPCI-2 C07H0021-04 [I,A]; C07H0021-00 [I,C\*]; C12N0001-20 [I,A];  
C12N0015-00 [I,A]; C12P0001-20 [I,A]  
IPCR C07H0021-00 [I,C]; C07H0021-04 [I,A]; C07K0014-195 [I,C\*];  
C07K0014-335 [I,A]; C12N0001-20 [I,C]; C12N0001-20 [I,A];  
C12N0001-21 [I,C\*]; C12N0001-21 [I,A]; C12N0009-00 [I,C\*];  
C12N0009-00 [I,A]; C12N0015-00 [I,C]; C12N0015-00 [I,A];  
C12P0021-06 [I,C\*]; C12P0021-06 [I,A]; C12Q0001-68 [I,C\*];  
C12Q0001-68 [I,A]  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 17 OF 27 USPATFULL on STN  
AN 2004:95339 USPATFULL  
TI Nutritional formulations containing synbiotic substances  
IN Kaup, Susan M., Collingswood, NJ, UNITED STATES  
Wilson, Jeffrey L., Doylestown, PA, UNITED STATES  
Kostek, Beverley M., Glen Mills, PA, UNITED STATES  
Frantz, David C., Pottstown, PA, UNITED STATES  
PA Wyeth, Madison, NJ, UNITED STATES, 07940 (U.S. corporation)  
PI US 20040072794 A1 20040415  
AI US 2003-681658 A1 20031008 (10)  
PRAI US 2002-418109P 20021011 (60)  
DT Utility  
FS APPLICATION  
LN.CNT 542  
INCL INCLM: 514/054.000  
INCLS: 424/093.450  
NCL NCLM: 514/054.000  
NCLS: 424/093.450  
IC [7]  
ICM A61K045-00  
ICS A61K031-715  
IPCI A61K0045-00 [ICM,7]; A61K0031-715 [ICS,7]  
IPCR A23L0001-052 [I,C\*]; A23L0001-0528 [I,A]; A23L0001-29 [I,C\*];  
A23L0001-29 [I,A]; A23L0001-30 [I,C\*]; A23L0001-30 [I,A]  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 18 OF 27 USPATFULL on STN  
AN 2004:12970 USPATFULL  
TI Polynucleotides, materials incorporating them, and methods for using  
them  
IN Glenn, Matthew, Whenuapai, NEW ZEALAND  
Havukkala, Ilkka J., Remuera, NEW ZEALAND  
Lubbers, Mark, Palmerston North, NEW ZEALAND  
Dekker, James, Palmerston North, NEW ZEALAND  
PA GENESIS RESEARCH AND DEVELOPMENT CORP. LTD., Parnell, NEW ZEALAND  
(non-U.S. corporation)  
PI US 20040009490 A1 20040115  
US 7125698 B2 20061024  
AI US 2002-264213 A1 20021003 (10)  
RLI Continuation-in-part of Ser. No. US 2001-971536, filed on 2 Oct 2001,  
PENDING Continuation-in-part of Ser. No. US 2000-634238, filed on 8 Aug  
2000, GRANTED, Pat. No. US 6544772

PRAI US 1999-147853P 19990809 (60)  
 US 1999-147852P 19990809 (60)  
 US 1999-152032P 19990901 (60)  
 US 1999-152031P 19990901 (60)  
 DT Utility  
 FS APPLICATION  
 LN.CNT 5375  
 INCL INCLM: 435/006.000  
 INCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.200  
 NCL NCLM: 435/193.000; 435/006.000  
 NCLS: 426/534.000; 435/183.000; 435/194.000; 530/350.000; 435/069.100;  
 435/252.300; 435/320.100; 536/023.200  
 IC [7]  
 ICM C12Q001-68  
 ICS C07H021-04; C12P021-02; C12N001-21; C12N015-74; C07K014-335  
 IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C\*];  
 C12P0021-02 [ICS,7]; C12N0001-21 [ICS,7]; C12N0015-74 [ICS,7];  
 C07K0014-335 [ICS,7]; C07K0014-195 [ICS,7,C\*]  
 IPCI-2 C12N0009-10 [I,A]  
 IPCR C12N0009-10 [I,C]; C12N0009-10 [I,A]; A23C0019-00 [I,C\*];  
 A23C0019-032 [I,A]; A61K0038-00 [N,C\*]; A61K0038-00 [N,A];  
 C07K0014-195 [I,C\*]; C07K0014-335 [I,A]; C12N0001-21 [I,C\*];  
 C12N0001-21 [I,A]  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 19 OF 27 USPATFULL on STN  
 AN 2004:250212 USPATFULL  
 TI Nucleic acid and amino acid sequences relating to Streptococcus  
 pneumoniae for diagnostics and therapeutics  
 IN Doucette-Stamm, Lynn A., Framingham, MA, United States  
 Bush, David, Somerville, MA, United States  
 PA Genome Therapeutics Corporation, Waltham, MA, United States (U.S.  
 corporation)  
 PI US 6800744 B1 20041005  
 AI US 1998-107433 19980630 (9)  
 PRAI US 1998-85131P 19980512 (60)  
 US 1997-51553P 19970702 (60)  
 DT Utility  
 FS GRANTED  
 LN.CNT 11545  
 INCL INCLM: 536/023.100  
 INCLS: 435/006.000; 435/320.100; 435/325.000; 435/254.000; 435/419.000;  
 536/024.100; 536/023.400; 536/024.320  
 NCL NCLM: 536/023.100  
 NCLS: 435/006.000; 435/320.100; 435/325.000; 435/419.000; 536/023.400;  
 536/024.100; 536/024.320  
 IC [7]  
 ICM C12Q001-68  
 ICS C12N001-14; C12N015-00; C12N005-00; C12N005-04; C07H021-02;  
 C07H021-04  
 IPCI C12Q0001-68 [ICM,7]; C12N0001-14 [ICS,7]; C12N0015-00 [ICS,7];  
 C12N0005-00 [ICS,7]; C12N0005-04 [ICS,7]; C07H0021-02 [ICS,7];  
 C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C\*]  
 IPCR C07H0021-00 [I,C\*]; C07H0021-02 [I,A]; C07H0021-04 [I,A];  
 C07K0014-195 [I,C\*]; C07K0014-315 [I,A]  
 EXF 536/23.1; 536/23.4; 536/24.32; 435/320.1; 435/325; 435/254.11; 435/419;  
 435/6  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 20 OF 27 USPATFULL on STN  
 AN 2003:71519 USPATFULL  
 TI Corynebacterium glutamicum genes encoding metabolic pathway proteins

IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF  
Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF  
Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF  
Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF  
Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF  
Kim, Jun-Won, Seoul, KOREA, REPUBLIC OF  
Lee, Heung-Shick, Seoul, KOREA, REPUBLIC OF  
Hwang, Byung-Joon, Seoul, KOREA, REPUBLIC OF

PI US 20030049804 A1 20030313  
AI US 2000-746660 A1 20001222 (9)

RLI Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,  
PENDING Continuation-in-part of Ser. No. US 2000-603124, filed on 23 Jun  
2000, PENDING

PRAI DE 1999-19931420 19990708  
US 1999-141031P 19990625 (60)  
US 1999-142101P 19990702 (60)  
US 1999-148613P 19990812 (60)  
US 2000-187970P 20000309 (60)

DT Utility  
FS APPLICATION

LN.CNT 15004

INCL INCLM: 435/115.000  
INCLS: 435/069.100; 435/252.300; 435/320.100; 435/183.000; 536/023.200

NCL NCLM: 435/115.000  
NCLS: 435/069.100; 435/183.000; 435/252.300; 435/320.100; 536/023.200

IC [7]  
ICM C12P013-08  
ICS C07H021-04; C12N009-00; C12P021-02; C12N001-21  
IPCI C12P0013-08 [ICM,7]; C12P0013-00 [ICM,7,C\*]; C07H0021-04 [ICS,7];  
C07H0021-00 [ICS,7,C\*]; C12N0009-00 [ICS,7]; C12P0021-02 [ICS,7];  
C12N0001-21 [ICS,7]  
IPCR C07K0014-195 [I,C\*]; C07K0014-34 [I,A]; C12N0001-21 [I,C\*];  
C12N0001-21 [I,A]; C12N0009-00 [I,C\*]; C12N0009-00 [I,A];  
C12N0009-18 [I,C\*]; C12N0009-18 [I,A]; C12N0009-90 [I,C\*];  
C12N0009-90 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 21 OF 27 USPATFULL on STN

AN 2003:95966 USPATFULL

TI Polynucleotides, materials incorporating them, and methods for using  
them

IN Glenn, Matthew, Auckland, NEW ZEALAND  
Havukkala, Ilkka J., Auckland, NEW ZEALAND  
Blokberg, Leonard N., Auckland, NEW ZEALAND  
Lubbers, Mark W., Palmerston North, NEW ZEALAND  
Dekker, James, Palmerston North, NEW ZEALAND  
Christensson, Anna C., Lund, SWEDEN  
Holland, Ross, Palmerston North, NEW ZEALAND  
O'Toole, Paul W., Palmerston North, NEW ZEALAND  
Reid, Julian R., Palmerston North, NEW ZEALAND  
Coolbear, Timothy, Palmerston North, NEW ZEALAND

PA Genesis Research & Development Corp. Ltd, Parnell, NEW ZEALAND (non-U.S.  
corporation)  
Via Lachia Bioscience (NZ) Ltd., Auckland, NEW ZEALAND (non-U.S.  
corporation)

PI US 6544772 B1 20030408  
AI US 2000-634238 20000808 (9)

DT Utility  
FS GRANTED

LN.CNT 2015

INCL INCLM: 435/252.300  
INCLS: 435/320.100; 536/023.700



NCL NCLM: 435/252.300  
 NCLS: 435/320.100; 536/023.700  
 IC [7]  
 ICM C12N001-21  
 ICS C12N015-63; C12N015-31  
 IPCI C12N0001-21 [ICM,7]; C12N0015-63 [ICS,7]; C12N0015-31 [ICS,7]  
 IPCR A23C0019-00 [I,C\*]; A23C0019-032 [I,A]; C07K0014-195 [I,C\*];  
 C07K0014-335 [I,A]; C12N0001-21 [I,C\*]; C12N0001-21 [I,A];  
 C12N0015-31 [I,C\*]; C12N0015-31 [I,A]  
 EXF 435/252.3; 435/320.1; 536/23.7  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 22 OF 27 BIOTECHDS COPYRIGHT 2008 THOMSON REUTERS on STN  
 AN 1999-00562 BIOTECHDS  
 TI Use of lactic and propionic acid bacteria;  
 to bind mycotoxin to prevent their absorption or to purify  
 contaminated food or feedstuff  
 AU El-Nezami H; Kankaanpaa P; Salminen S; Ahokas J  
 PA Roy.Melbourne-Inst.Technol.  
 LO Melbourne, Victoria, Australia.  
 PI WO 9834503 13 Aug 1998  
 AI WO 1998-AU63 6 Feb 1998  
 PRAI AU 1997-5005 7 Feb 1997  
 DT Patent  
 LA English  
 OS WPI: 1998-557001 [49]

L5 ANSWER 23 OF 27 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): CP000705 GenBank (R)  
 GenBank ACC. NO. (GBN): CP000705 AAOV01000000 AAOV01000001-AAOV01000097  
 GenBank VERSION (VER): CP000705.1 GI:148530277  
 SEQUENCE LENGTH (SQL): 1999618  
 MOLECULE TYPE (CI): DNA; circular  
 DIVISION CODE (CI): Bacteria  
 DATE (DATE): 17 Oct 2007  
 DEFINITION (DEF): Lactobacillus reuteri F275,  
 complete genome.  
 SOURCE: Lactobacillus reuteri F275  
 ORGANISM (ORGN): Lactobacillus reuteri F275  
 Bacteria; Firmicutes; Lactobacillales;  
 Lactobacillaceae; Lactobacillus  
 PROJECT (PJID): GenomeProject:15766  
 COMMENT:  
 URL -- <http://www.jgi.doe.gov>  
 JGI Project ID: 4000135  
 Source DNA available from Gerald Tannock  
 (gerald.tannock@stonebow.otago.ac.nz)  
 Bacteria available from DSMZ: DSM 20016  
 Contacts: Gerald Tannock (gerald.tannock@stonebow.otago.ac.nz)  
 Paul Richardson (microbes@cuba.jgi-psf.org)  
 Quality assurance done by JGI-Stanford  
 Annotation done by JGI-ORNL and JGI-PGF  
 Finishing done by JGI-PGF  
 Finished microbial genomes have been curated to close all gaps with  
 greater than 98% coverage of at least two independent clones. Each  
 base pair has a minimum q (quality) value of 30 and the total error  
 rate is less than one per 50000.  
 The JGI and collaborators endorse the principles for the  
 distribution and use of large scale sequencing data adopted by the  
 larger genome sequencing community and urge users of this data to  
 follow them. It is our intention to publish the work of this

project in a timely fashion and we welcome collaborative interaction on the project and analysis.

(<http://www.genome.gov/page.cfm?pageID=10506376>).

REFERENCE: 1 (bases 1 to 1999618)  
AUTHOR (AU): Copeland,A.; Lucas,S.; Lapidus,A.; Barry,K.;  
Detter,J.C.; Glavina del Rio,T.; Hammon,N.; Israni,S.;  
Dalin,E.; Tice,H.; Pitluck,S.; Goltsman,E.; Schmutz,J.;  
Larimer,F.; Land,M.; Hauser,L.; Kyrpides,N.; Kim,E.;  
Walter,J.; Heng,N.C.K.; Tannock,G.W.; Richardson,P.  
TITLE (TI): Complete sequence of chromosome of  
Lactobacillus reuteri DSM 20016  
JOURNAL (SO): Unpublished  
REFERENCE: 2 (bases 1 to 1999618)  
AUTHOR (AU): Copeland,A.; Lucas,S.; Lapidus,A.; Barry,K.;  
Detter,J.C.; Glavina del Rio,T.; Hammon,N.; Israni,S.;  
Dalin,E.; Tice,H.; Pitluck,S.; Goltsman,E.; Schmutz,J.;  
Larimer,F.; Land,M.; Hauser,L.; Kyrpides,N.; Kim,E.;  
Walter,J.; Heng,N.C.K.; Tannock,G.W.; Richardson,P.  
TITLE (TI): Direct Submission  
JOURNAL (SO): Submitted (17-MAY-2007) US DOE Joint Genome Institute,  
2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698,  
USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1999618	/organism="Lactobacillus reuteri F275" /mol-type="genomic DNA" /strain="DSM 20016" /db-xref="taxon:299033" /note="F275 = DSM 20016 = JCM 1112"

L5 ANSWER 24 OF 27 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): AM270397 GenBank (R)  
GenBank ACC. NO. (GBN): AM270397  
GenBank VERSION (VER): AM270397.1 GI:134084136  
CAS REGISTRY NO. (RN): 928607-03-8  
SEQUENCE LENGTH (SQL): 163680  
MOLECULE TYPE (CI): DNA; linear  
DIVISION CODE (CI): Plants, fungi, algae  
DATE (DATE): 24 Mar 2007  
DEFINITION (DEF): Aspergillus niger contig An18c0040, complete genome.  
SOURCE: Aspergillus niger  
ORGANISM (ORGN): Aspergillus niger  
Eukaryota; Fungi; Ascomycota; Pezizomycotina;  
Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic  
Trichocomaceae; Aspergillus  
REFERENCE: 1 (bases 150631 to 153085)  
AUTHOR (AU): Habison,A.; Kubicek,C.P.; Rohr,M.  
TITLE (TI): Partial purification and regulatory properties of  
phosphofructokinase from Aspergillus niger  
JOURNAL (SO): Biochem. J., 209 (3), 669-676 (1983)  
OTHER SOURCE (OS): CA 99:171737  
REFERENCE: 2 (bases 71863 to 73356)  
AUTHOR (AU): Manney,T.R.  
TITLE (TI): Expression of the BAR1 gene in Saccharomyces  
cerevisiae: induction by the alpha mating pheromone of  
an activity associated with a secreted protein

JOURNAL (SO): J. Bacteriol., 155 (1), 291-301 (1983)  
 OTHER SOURCE (OS): CA 99:102121  
 REFERENCE: 3 (bases 71863 to 73356)  
 AUTHOR (AU): Jones, E.W.  
 TITLE (TI): The synthesis and function of proteases in  
 Saccharomyces: genetic approaches  
 JOURNAL (SO): Annu. Rev. Genet., 18, 233-270 (1984)  
 OTHER SOURCE (OS): CA 102:92538  
 REFERENCE: 4 (bases 144032 to 145578)  
 AUTHOR (AU): Brandsch, R.; Bichler, V.  
 TITLE (TI): In vivo and in vitro expression of the  
 6-hydroxy-D-nicotine oxidase gene of Arthrobacter  
 oxidans, cloned into Escherichia coli, as an  
 enzymatically active, covalently flavinylated  
 polypeptide  
 JOURNAL (SO): FEBS Lett., 192 (2), 204-208 (1985)  
 OTHER SOURCE (OS): CA 104:29597  
 REFERENCE: 5 (bases 150631 to 153085)  
 AUTHOR (AU): Schrefler, G.; Kubicek, C.P.; Rohr, M.  
 TITLE (TI): Inhibition of citric acid accumulation by manganese  
 ions in Aspergillus niger mutants with reduced citrate  
 control of phosphofructokinase  
 JOURNAL (SO): J. Bacteriol., 165 (3), 1019-1022 (1986)  
 OTHER SOURCE (OS): CA 104:165023  
 REFERENCE: 6 (bases 156827 to 158638)  
 AUTHOR (AU): Whittington, H.A.; Grant, S.; Roberts, C.F.; Lamb, H.;  
 Hawkins, A.R.  
 TITLE (TI): Identification and isolation of a putative permease  
 gene in the quinic acid utilization (QUT) gene cluster  
 of Aspergillus nidulans  
 JOURNAL (SO): Curr. Genet., 12 (2), 135-139 (1987)  
 OTHER SOURCE (OS): CA 107:91128  
 REFERENCE: 7 (bases 54105 to 55762)  
 AUTHOR (AU): Chisholm, V.T.; Lea, H.Z.; Rai, R.; Cooper, T.G.  
 TITLE (TI): Regulation of allantate transport in wild-type and  
 mutant strains of Saccharomyces cerevisiae  
 JOURNAL (SO): J. Bacteriol., 169 (4), 1684-1690 (1987)  
 OTHER SOURCE (OS): CA 106:172689  
 REFERENCE: 8 (bases 71863 to 73356)  
 AUTHOR (AU): MacKay, V.L.; Welch, S.K.; Insley, M.Y.; Manney, T.R.;  
 Holly, J.; Saari, G.C.; Parker, M.L.  
 TITLE (TI): The Saccharomyces cerevisiae BAR1 gene encodes an  
 exported protein with homology to pepsin  
 JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 85 (1), 55-59 (1988)  
 OTHER SOURCE (OS): CA 108:125658  
 REFERENCE: 9 (bases 54105 to 55762)  
 AUTHOR (AU): Rai, R.; Genbauffe, F.S.; Cooper, T.G.  
 TITLE (TI): Structure and transcription of the allantate permease  
 gene (DAL5) from Saccharomyces cerevisiae  
 JOURNAL (SO): J. Bacteriol., 170 (1), 266-271 (1988)  
 OTHER SOURCE (OS): CA 109:17930  
 REFERENCE: 10  
 AUTHOR (AU): Hawkins, A.R.; Lamb, H.K.; Smith, M.; Keyte, J.W.;  
 Roberts, C.F.  
 TITLE (TI): Molecular organisation of the quinic acid utilization  
 (QUT) gene cluster in Aspergillus nidulans  
 JOURNAL (SO): Mol. Gen. Genet., 214 (2), 224-231 (1988)  
 OTHER SOURCE (OS): CA 111:188522  
 REFERENCE: 11 (bases 68231 to 69040)  
 AUTHOR (AU): Honjo, M.; Nakayama, A.; Fukazawa, K.; Kawamura, K.;  
 Ando, K.; Furutani, Y.  
 TITLE (TI): A novel Bacillus subtilis gene involved in negative

control of sporulation and degradative-enzyme  
production

JOURNAL (SO): J. Bacteriol., 172 (4), 1783-1790 (1990)  
OTHER SOURCE (OS): CA 113:146166  
REFERENCE: 12 (bases 5212 to 7379)  
AUTHOR (AU): Nikawa,J.; Hosaka,K.; Tsukagoshi,Y.; Yamashita,S.  
TITLE (TI): Primary structure of the yeast choline transport gene  
and regulation of its expression

JOURNAL (SO): J. Biol. Chem., 265 (26), 15996-16003 (1990)  
OTHER SOURCE (OS): CA 114:18549  
REFERENCE: 13 (bases 159975 to 161849)  
AUTHOR (AU): Fling,M.E.; Kopf,J.; Tamarkin,A.; Gorman,J.A.;  
Smith,H.A.; Koltin,Y.  
TITLE (TI): Analysis of a *Candida albicans* gene that encodes a  
novel mechanism for resistance to benomyl and  
methotrexate

JOURNAL (SO): Mol. Gen. Genet., 227 (2), 318-329 (1991)  
OTHER SOURCE (OS): CA 116:100405  
REFERENCE: 14 (bases 28874 to 30837)  
AUTHOR (AU): Masuda,N.; Kitamura,N.; Saito,K.  
TITLE (TI): Primary structure of protein moiety of *Penicillium*  
*notatum* phospholipase B deduced from the cDNA

JOURNAL (SO): Eur. J. Biochem., 202 (3), 783-787 (1991)  
OTHER SOURCE (OS): CA 118:76020  
REFERENCE: 15 (bases 100363 to 101496)  
AUTHOR (AU): Sakoda,H.; Imanaka,T.  
TITLE (TI): Cloning and sequencing of the gene coding for alcohol  
dehydrogenase of *Bacillus stearothermophilus* and  
rational shift of the optimum pH

JOURNAL (SO): J. Bacteriol., 174 (4), 1397-1402 (1992)  
OTHER SOURCE (OS): CA 118:186708  
REFERENCE: 16 (bases 20773 to 22555)  
AUTHOR (AU): Kamoda,S.; Saburi,Y.  
TITLE (TI): Structural and enzymatical comparison of  
lignostilbene- $\alpha$ , $\beta$ -dioxygenase isozymes, I, II,  
and III, from *Pseudomonas paucimobilis* TMY1009

JOURNAL (SO): Biosci. Biotechnol. Biochem., 57 (6), 931-934 (1993)  
OTHER SOURCE (OS): CA 119:154577  
REFERENCE: 17 (bases 80602 to 83154)  
AUTHOR (AU): ElBerry,H.M.; Majumdar,M.L.; Cunningham,T.S.;  
Sumrada,R.A.; Cooper,T.G.  
TITLE (TI): Regulation of the urea active transporter gene (DUR3)  
in *Saccharomyces cerevisiae*

JOURNAL (SO): J. Bacteriol., 175 (15), 4688-4698 (1993)  
OTHER SOURCE (OS): CA 119:242524  
REFERENCE: 18 (bases 23096 to 24052)  
AUTHOR (AU): Roper,D.I.; Cooper,R.A.  
TITLE (TI): Purification, nucleotide sequence and some properties  
of a bifunctional isomerase/decarboxylase from the  
homoprotocatechuate degradative pathway of *Escherichia*  
*coli* C

JOURNAL (SO): Eur. J. Biochem., 217 (2), 575-580 (1993)  
OTHER SOURCE (OS): CA 119:265270  
REFERENCE: 19 (bases 5212 to 7379)  
AUTHOR (AU): Li,Z.; Brendel,M.  
TITLE (TI): Co-regulation with genes of phospholipid biosynthesis  
of the CTR/HNM1-encoded choline/nitrogen mustard  
permease in *Saccharomyces cerevisiae*

JOURNAL (SO): Mol. Gen. Genet., 241 (5-6), 680-684 (1993)  
OTHER SOURCE (OS): CA 121:28475  
REFERENCE: 20 (bases 159975 to 161849)  
AUTHOR (AU): Ben-Yaacov,R.; Knoller,S.; Caldwell,G.A.; Becker,J.M.;

Koltin,Y.  
 TITLE (TI): Candida albicans gene encoding resistance to benomyl  
 and methotrexate is a multidrug resistance gene  
 JOURNAL (SO): Antimicrob. Agents Chemother., 38 (4), 648-652 (1994)  
 OTHER SOURCE (OS): CA 121:2236  
 REFERENCE: 21 (bases 150631 to 153085)  
 AUTHOR (AU): Legisa,M.; Bencina,M.  
 TITLE (TI): Evidence for the activation of 6-phosphofructo-1-kinase  
 by cAMP-dependent protein kinase in Aspergillus niger  
 JOURNAL (SO): FEMS Microbiol. Lett., 118 (3), 327-333 (1994)  
 OTHER SOURCE (OS): CA 121:102759  
 REFERENCE: 22 (bases 138020 to 140061)  
 AUTHOR (AU): Kim,Y.J.; Bjorklund,S.; Li,Y.; Sayre,M.H.;  
 Kornberg,R.D.  
 TITLE (TI): A multiprotein mediator of transcriptional activation  
 and its interaction with the C-terminal repeat domain  
 of RNA polymerase II  
 JOURNAL (SO): Cell, 77 (4), 599-608 (1994)  
 OTHER SOURCE (OS): CA 121:102149  
 REFERENCE: 23 (bases 38805 to 39836)  
 AUTHOR (AU): Downs,D.M.; Petersen,L.  
 TITLE (TI): apbA, a new genetic locus involved in thiamine  
 biosynthesis in Salmonella typhimurium  
 JOURNAL (SO): J. Bacteriol., 176 (16), 4858-4864 (1994)  
 OTHER SOURCE (OS): CA 121:197350  
 REFERENCE: 24 (bases 5212 to 7379)  
 AUTHOR (AU): Li,Z.; Brendel,M.  
 TITLE (TI): Sensitivity to nitrogen mustard in Saccharomyces  
 cerevisiae is independently determined by regulated  
 choline permease and DNA repair  
 JOURNAL (SO): Mutat. Res., 315 (2), 139-145 (1994)  
 OTHER SOURCE (OS): CA 121:198201  
 REFERENCE: 25 (bases 85096 to 90863)  
 AUTHOR (AU): Szczypka,M.S.; Wemmie,J.A.; Moye-Rowley,W.S.;  
 Thiele,D.J.  
 TITLE (TI): A yeast metal resistance protein similar to human  
 cystic fibrosis transmembrane conductance regulator  
 (CFTR) and multidrug resistance-associated protein  
 JOURNAL (SO): J. Biol. Chem., 269 (36), 22853-22857 (1994)  
 OTHER SOURCE (OS): CA 122:26140  
 REFERENCE: 26 (bases 91484 to 93088)  
 AUTHOR (AU): Knight,S.A.; Tamai,K.T.; Kosman,D.J.; Thiele,D.J.  
 TITLE (TI): Identification and analysis of a Saccharomyces  
 cerevisiae copper homeostasis gene encoding a  
 homeodomain protein  
 JOURNAL (SO): Mol. Cell. Biol., 14 (12), 7792-7804 (1994)  
 OTHER SOURCE (OS): CA 122:73697  
 REFERENCE: 27 (bases 85096 to 90863)  
 AUTHOR (AU): Wemmie,J.A.; Szczypka,M.S.; Thiele,D.J.;  
 Moye-Rowley,W.S.  
 TITLE (TI): Cadmium tolerance mediated by the yeast AP-1 protein  
 requires the presence of an ATP-binding cassette  
 transporter-encoding gene, YCF1  
 JOURNAL (SO): J. Biol. Chem., 269 (51), 32592-32597 (1994)  
 OTHER SOURCE (OS): CA 121:294343  
 REFERENCE: 28 (bases 20773 to 22555)  
 AUTHOR (AU): Kamoda,S.; Saburi,Y.  
 TITLE (TI): Cloning of a lignostilbene-alpha,beta-dioxygenase  
 isozyme gene from Pseudomonas paucimobilis TMY1009  
 JOURNAL (SO): Biosci. Biotechnol. Biochem., 59 (10), 1866-1868 (1995)  
 OTHER SOURCE (OS): CA 124:47043  
 REFERENCE: 29 (bases 85096 to 90863)

AUTHOR (AU): Li,Z.S.; Szczypka,M.; Lu,Y.P.; Thiele,D.J.; Rea,P.A.  
 TITLE (TI): The yeast cadmium factor protein (YCF1) is a vacuolar glutathione S-conjugate pump  
 JOURNAL (SO): J. Biol. Chem., 271 (11), 6509-6517 (1996)  
 OTHER SOURCE (OS): CA 124:226108  
 REFERENCE: 30 (bases 33419 to 35477)  
 AUTHOR (AU): Silva,J.C.; Minto,R.E.; Barry,C.E. III; Holland,K.A.; Townsend,C.A.  
 TITLE (TI): Isolation and characterization of the versicolorin B synthase gene from *Aspergillus parasiticus*. Expansion of the aflatoxin b1 biosynthetic gene cluster  
 JOURNAL (SO): J. Biol. Chem., 271 (23), 13600-13608 (1996)  
 OTHER SOURCE (OS): CA 125:50401  
 REFERENCE: 31 (bases 15614 to 17392)  
 AUTHOR (AU): Covert,S.F.; Enkerli,J.; Miao,V.P.; VanEtten,H.D.  
 TITLE (TI): A gene for maackiain detoxification from a dispensable chromosome of *Nectria haematococca*  
 JOURNAL (SO): Mol. Gen. Genet., 251 (4), 397-406 (1996)  
 OTHER SOURCE (OS): CA 125:106677  
 REFERENCE: 32 (bases 131646 to 132375)  
 AUTHOR (AU): Mitsuhashi,S.; Miyachi,S.  
 TITLE (TI): Amino acid sequence homology between N- and C-terminal halves of a carbonic anhydrase in *Porphyridium purpureum*, as deduced from the cloned cDNA  
 JOURNAL (SO): J. Biol. Chem., 271 (45), 28703-28709 (1996)  
 OTHER SOURCE (OS): CA 125:321312  
 REFERENCE: 33 (bases 85096 to 90863)  
 AUTHOR (AU): Li,Z.S.; Lu,Y.P.; Zhen,R.G.; Szczypka,M.; Thiele,D.J.; Rea,P.A.  
 TITLE (TI): A new pathway for vacuolar cadmium sequestration in *Saccharomyces cerevisiae*: YCF1-catalyzed transport of bis(glutathionato)cadmium  
 JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 94 (1), 42-47 (1997)  
 OTHER SOURCE (OS): CA 126:127966  
 REFERENCE: 34 (bases 1241 to 3043)  
 AUTHOR (AU): Saito,Y.; Ishii,Y.; Hayashi,H.; Imao,Y.; Akashi,T.; Yoshikawa,K.; Noguchi,Y.; Soeda,S.; Yoshida,M.; Niwa,M.; Hosoda,J.; Shimomura,K.  
 TITLE (TI): Cloning of genes coding for L-sorbose and L-sorbose dehydrogenases from *Gluconobacter oxydans* and microbial production of 2-keto-L-gulonate, a precursor of L-ascorbic acid, in a recombinant *G. oxydans* strain  
 JOURNAL (SO): Appl. Environ. Microbiol., 63 (2), 454-460 (1997)  
 OTHER SOURCE (OS): CA 126:167180  
 REFERENCE: 35 (bases 150631 to 153085)  
 AUTHOR (AU): Ruijter,G.J.; Panneman,H.; Visser,J.  
 TITLE (TI): Overexpression of phosphofructokinase and pyruvate kinase in citric acid-producing *Aspergillus niger*  
 JOURNAL (SO): Biochim. Biophys. Acta, 1334 (2-3), 317-326 (1997)  
 OTHER SOURCE (OS): CA 126:222695  
 REFERENCE: 36 (bases 49850 to 51919)  
 AUTHOR (AU): Prieto,R.; Woloshuk,C.P.  
 TITLE (TI): *ord1*, an oxidoreductase gene responsible for conversion of O-methylsterigmatocystin to aflatoxin in *Aspergillus flavus*  
 JOURNAL (SO): Appl. Environ. Microbiol., 63 (5), 1661-1666 (1997)  
 OTHER SOURCE (OS): CA 127:13942  
 REFERENCE: 37 (bases 17766 to 20491)  
 AUTHOR (AU): Todd,R.B.; Murphy,R.L.; Martin,H.M.; Sharp,J.A.; Davis,M.A.; Katz,M.E.; Hynes,M.J.  
 TITLE (TI): The acetate regulatory gene *facB* of *Aspergillus nidulans* encodes a Zn(II)2Cys6 transcriptional

activator

JOURNAL (SO): Mol. Gen. Genet., 254 (5), 495-504 (1997)

OTHER SOURCE (OS): CA 127:105007

REFERENCE: 38 (bases 71863 to 73356)

AUTHOR (AU): Ballensiefen,W.; Schmitt,H.D.

TITLE (TI): Periplasmic Bar1 protease of *Saccharomyces cerevisiae* is active before reaching its extracellular destination

JOURNAL (SO): Eur. J. Biochem., 247 (1), 142-147 (1997)

OTHER SOURCE (OS): CA 127:187926

REFERENCE: 39 (bases 52148 to 53720)

AUTHOR (AU): Kuroyanagi,N.; Onogi,H.; Wakabayashi,T.; Hagiwara,M.

TITLE (TI): Novel SR-protein-specific kinase, SRPK2, disassembles nuclear speckles

JOURNAL (SO): Biochem. Biophys. Res. Commun., 242 (2), 357-364 (1998)

OTHER SOURCE (OS): CA 128:241040

REFERENCE: 40 (bases 113565 to 114733)

AUTHOR (AU): MacDiarmid,C.W.; Gardner,R.C.

TITLE (TI): Overexpression of the *Saccharomyces cerevisiae* magnesium transport system confers resistance to aluminum ion

JOURNAL (SO): J. Biol. Chem., 273 (3), 1727-1732 (1998)

OTHER SOURCE (OS): CA 128:177021

REFERENCE: 41 (bases 135940 to 137166)

AUTHOR (AU): Wang,H.Y.; Lin,W.; Dyck,J.A.; Yeakley,J.M.; Songyang,Z.; Cantley,L.C.; Fu,X.D.

TITLE (TI): SRPK2: a differentially expressed SR protein-specific kinase involved in mediating the interaction and localization of pre-mRNA splicing factors in mammalian cells

JOURNAL (SO): J. Cell Biol., 140 (4), 737-750 (1998)

OTHER SOURCE (OS): CA 128:306636

REFERENCE: 42 (bases 38805 to 39836)

AUTHOR (AU): Frodyma,M.E.; Downs,D.

TITLE (TI): ApbA, the ketopantoate reductase enzyme of *Salmonella typhimurium* is required for the synthesis of thiamine via the alternative pyrimidine biosynthetic pathway

JOURNAL (SO): J. Biol. Chem., 273 (10), 5572-5576 (1998)

OTHER SOURCE (OS): CA 128:305459

REFERENCE: 43 (bases 106231 to 106803)

AUTHOR (AU): Woloshuk,C.P.; Prieto,R.

TITLE (TI): Genetic organization and function of the aflatoxin B1 biosynthetic genes

JOURNAL (SO): FEMS Microbiol. Lett., 160 (2), 169-176 (1998)

OTHER SOURCE (OS): CA 128:290649

REFERENCE: 44 (bases 93571 to 94963)

AUTHOR (AU): Philp,N.J.; Yoon,H.; Grollman,E.F.

TITLE (TI): Monocarboxylate transporter MCT1 is located in the apical membrane and MCT3 in the basal membrane of rat RPE

JOURNAL (SO): Am. J. Physiol., 274 (6 PT 2), R1824-R1828 (1998)

OTHER SOURCE (OS): CA 129:159493

REFERENCE: 45 (bases 93571 to 94963)

AUTHOR (AU): Wilson,M.C.; Jackson,V.N.; Heddle,C.; Price,N.T.; Pilegaard,H.; Juel,C.; Bonen,A.; Montgomery,I.; Hutter,O.F.; Halestrap,A.P.

TITLE (TI): Lactic acid efflux from white skeletal muscle is catalyzed by the monocarboxylate transporter isoform MCT3

JOURNAL (SO): J. Biol. Chem., 273 (26), 15920-15926 (1998)

OTHER SOURCE (OS): CA 129:159801

REFERENCE: 46 (bases 153410 to 154508)

AUTHOR (AU): Dekkers,L.C.; van der Bij,A.J.; Mulders,I.H.;

Phoelich, C.C.; Wentwoord, R.A.; Glandorf, D.C.;  
Wijffelman, C.A.; Lugtenberg, B.J.

TITLE (TI): Role of the O-antigen of lipopolysaccharide, and  
possible roles of growth rate and of NADH:ubiquinone  
oxidoreductase (nuo) in competitive tomato root-tip  
colonization by *Pseudomonas fluorescens* WCS365

JOURNAL (SO): *Mol. Plant Microbe Interact.*, 11 (8), 763-771 (1998)

OTHER SOURCE (OS): CA 129:200426

REFERENCE: 47 (bases 146433 to 148685)

AUTHOR (AU): Saito, K.; Yamazaki, H.; Ohnishi, Y.; Fujimoto, S.;  
Takahashi, E.; Horinouchi, S.

TITLE (TI): Production of trehalose synthase from a basidiomycete,  
*Grifola frondosa*, in *Escherichia coli*

JOURNAL (SO): *Appl. Microbiol. Biotechnol.*, 50 (2), 193-198 (1998)

OTHER SOURCE (OS): CA 130:956

REFERENCE: 48 (bases 122486 to 123895)

AUTHOR (AU): Kimura, M.; Matsumoto, G.; Shingu, Y.; Yoneyama, K.;  
Yamaguchi, I.

TITLE (TI): The mystery of the trichothecene 3-O-acetyltransferase  
gene. Analysis of the region around Tri101 and  
characterization of its homologue from *Fusarium*  
*sporotrichioides*

JOURNAL (SO): *FEBS Lett.*, 435 (2-3), 163-168 (1998)

OTHER SOURCE (OS): CA 130:11163

REFERENCE: 49 (bases 146433 to 148685)

AUTHOR (AU): Saito, K.; Kase, T.; Takahashi, E.; Horinouchi, S.

TITLE (TI): Purification and characterization of a trehalose  
synthase from the basidiomycete *grifola frondosa*

JOURNAL (SO): *Appl. Environ. Microbiol.*, 64 (11), 4340-4345 (1998)

OTHER SOURCE (OS): CA 130:34870

REFERENCE: 50 (bases 14029 to 15172)

AUTHOR (AU): Feng, Y.; Khoo, H.E.; Poh, C.L.

TITLE (TI): Purification and characterization of gentisate  
1,2-dioxygenases from *Pseudomonas alcaligenes* NCIB 9867  
and *Pseudomonas putida* NCIB 9869

JOURNAL (SO): *Appl. Environ. Microbiol.*, 65 (3), 946-950 (1999)

OTHER SOURCE (OS): CA 130:322223

REFERENCE: 51 (bases 59070 to 60560)

AUTHOR (AU): Bosch, R.; Moore, E.R.; Garcia-Valdes, E.; Pieper, D.H.

TITLE (TI): NahW, a novel, inducible salicylate hydroxylase  
involved in mineralization of naphthalene by  
*Pseudomonas stutzeri* AN10

JOURNAL (SO): *J. Bacteriol.*, 181 (8), 2315-2322 (1999)

OTHER SOURCE (OS): CA 131:70144

REFERENCE: 52

AUTHOR (AU): DeZwaan, T.M.; Carroll, A.M.; Valent, B.; Sweigard, J.A.

TITLE (TI): *Magnaporthe grisea* pth11p is a novel plasma membrane  
protein that mediates appressorium differentiation in  
response to inductive substrate cues

JOURNAL (SO): *Plant Cell*, 11 (10), 2013-2030 (1999)

OTHER SOURCE (OS): CA 132:47358

REFERENCE: 53 (bases 122486 to 123895)

AUTHOR (AU): McCormick, S.P.; Alexander, N.J.; Trapp, S.E.; Hohn, T.M.

TITLE (TI): Disruption of TRI101, the gene encoding trichothecene  
3-O-acetyltransferase, from *Fusarium sporotrichioides*

JOURNAL (SO): *Appl. Environ. Microbiol.*, 65 (12), 5252-5256 (1999)

OTHER SOURCE (OS): CA 132:118174

REFERENCE: 54 (bases 111907 to 113460)

AUTHOR (AU): Muraguchi, H.; Kamada, T.

TITLE (TI): A mutation in the *eln2* gene encoding a cytochrome P450  
of *Coprinus cinereus* affects mushroom morphogenesis

JOURNAL (SO): *Fungal Genet. Biol.*, 29 (1), 49-59 (2000)



OTHER SOURCE (OS): CA 134:96073

REFERENCE: 55 (bases 108826 to 111209)

AUTHOR (AU): Yu, J.; Chang, P.K.; Bhatnagar, D.; Cleveland, T.E.

TITLE (TI): Genes encoding cytochrome P450 and monooxygenase enzymes define one end of the aflatoxin pathway gene cluster in *Aspergillus parasiticus*

JOURNAL (SO): Appl. Microbiol. Biotechnol., 53 (5), 583-590 (2000)

OTHER SOURCE (OS): CA 133:291807

REFERENCE: 56 (bases 122486 to 123895)

AUTHOR (AU): Muhitch, M.J.; McCormick, S.P.; Alexander, N.J.; Hohn, T.M.

TITLE (TI): Transgenic expression of the TRI101 or PDR5 gene increases resistance of tobacco to the phytotoxic effects of the trichothecene 4,15-diacetoxyscirpenol

JOURNAL (SO): Plant Sci., 157 (2), 201-207 (2000)

OTHER SOURCE (OS): CA 133:306551

REFERENCE: 57 (bases 107279 to 108340)

AUTHOR (AU): Cheng, Q.; Thomas, S.M.; Kostichka, K.; Valentine, J.R.; Nagarajan, V.

TITLE (TI): Genetic analysis of a gene cluster for cyclohexanol oxidation in *Acinetobacter* sp. Strain SE19 by in vitro transposition

JOURNAL (SO): J. Bacteriol., 182 (17), 4744-4751 (2000)

OTHER SOURCE (OS): CA 134:37832

REFERENCE: 58 (bases 100363 to 101496)

AUTHOR (AU): Jornvall, H.; Hoog, J.O.; Persson, B.; Pares, X.

TITLE (TI): Pharmacogenetics of the alcohol dehydrogenase system

JOURNAL (SO): Pharmacology, 61 (3), 184-191 (2000)

OTHER SOURCE (OS): CA 134:38655

REFERENCE: 59

AUTHOR (AU): Calabrese, D.; Bille, J.; Sanglard, D.

TITLE (TI): A novel multidrug efflux transporter gene of the major facilitator superfamily from *Candida albicans* (FLU1) conferring resistance to fluconazole

JOURNAL (SO): Microbiology (Reading, Engl.), 146 (PT 11), 2743-2754 (2000)

OTHER SOURCE (OS): CA 135:1055

REFERENCE: 60

AUTHOR (AU): Deising, H.B.; Werner, S.; Wernitz, M.

TITLE (TI): The role of fungal appressoria in plant infection

JOURNAL (SO): Microbes Infect., 2 (13), 1631-1641 (2000)

REFERENCE: 61 (bases 43783 to 45994)

AUTHOR (AU): Smith, S.

TITLE (TI): The world according to PARP

JOURNAL (SO): Trends Biochem. Sci., 26 (3), 174-179 (2001)

OTHER SOURCE (OS): CA 135:15779

REFERENCE: 62 (bases 131646 to 132375)

AUTHOR (AU): Cronk, J.D.; Endrizzi, J.A.; Cronk, M.R.; O'Neill, J.W.; Zhang, K.Y.

TITLE (TI): Crystal structure of *E. coli* beta-carbonic anhydrase, an enzyme with an unusual pH-dependent activity

JOURNAL (SO): Protein Sci., 10 (5), 911-922 (2001)

REFERENCE: 63 (bases 43783 to 45994)

AUTHOR (AU): Ziegler, M.; Oei, S.L.

TITLE (TI): A cellular survival switch: poly(ADP-ribosyl)ation stimulates DNA repair and silences transcription

JOURNAL (SO): Bioessays, 23 (6), 543-548 (2001)

REFERENCE: 64 (bases 43783 to 45994)

AUTHOR (AU): Herceg, Z.; Wang, Z.Q.

TITLE (TI): Functions of poly(ADP-ribose) polymerase (PARP) in DNA repair, genomic integrity and cell death

JOURNAL (SO): Mutat. Res., 477 (1-2), 97-110 (2001)

OTHER SOURCE (OS): CA 136:145570

REFERENCE: 65 (bases 15614 to 17392)  
 AUTHOR (AU): Mundodi, S.R.; Watson, B.S.; Lopez-Meyer, M.; Paiva, N.L.  
 TITLE (TI): Functional expression and subcellular localization of  
 the *Nectria haematococca* Mak1 phytoalexin  
 detoxification enzyme in transgenic tobacco  
 JOURNAL (SO): Plant Mol. Biol., 46 (4), 421-432 (2001)  
 OTHER SOURCE (OS): CA 135:285870  
 REFERENCE: 66 (bases 1 to 163680)  
 AUTHOR (AU): Pel, H.J.; de Winde, J.H.; Archer, D.B.; Dyer, P.S.;  
 Hofmann, G.; Schaap, P.J.; Turner, G.; de Vries, R.P.;  
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 van Dijk, A.; Dijkhuizen, L.; Driessen, A.J.; d'Enfert, C.;  
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 Vervecken, W.; van de Vondervoort, P.J.; Wedler, H.;  
 Wosten, H.A.; Zeng, A.P.; van Ooyen, A.J.; Visser, J.;  
 Stam, H.  
 TITLE (TI): Genome sequencing and analysis of the versatile cell  
 factory *Aspergillus niger* CBS 513.88  
 JOURNAL (SO): Nat. Biotechnol., 25 (2), 221-231 (2007)  
 OTHER SOURCE (OS): CA 146:310276  
 REFERENCE: 67 (bases 1 to 163680)  
 AUTHOR (AU): Pel, H.J.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (01-MAY-2006) Pel H.J., DSM, 624-0295, P.O.  
 Box 1, 2600 MA Delft, THE NETHERLANDS

# FEATURES (FEAT):

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	4678..4775))	
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		TETGRVAGGCEWLIFHKNPFPNGP
		QPLSCTWYPEGSERAHEYASRMLSQAFFPRMCWLQ
		RPHAGVNAMEGVHPDYRRRGVGRLL
		MQWGERIDPLGYESWIEGSPIGRWLYEESGYKR
		VISLNIDFAKKNPSEWNRLVHEC
		QPPAILLLWRPPRGWENDKVPPGPWAVTEDTWK"
exon	complement(3788..4122)	/locus-tag="An18g00950"
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intron	complement(4123..4200)	/locus-tag="An18g00950"
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exon	complement(4678..4775)	/locus-tag="An18g00950"
		/number=3
gene	complement(<5212..>7379	/locus-tag="An18g00960"
	)	
mRNA	complement(join(<5212..	/locus-tag="An18g00960"
	5456,5493..5664,	
	5746..6075,6140..6159,	
	6225..6602,6674..6746,	
	6800..6899,	
	7249..>7379))	
CDS	complement(join(5212..5	/locus-tag="An18g00960"
	456,5493..5664,	
	5746..6075,6140..6159,	
	6225..6602,6674..6746,	
	6800..6899,7249..7379))	
		/inference="profile:COGS:COG0833"
		/inference="similar to AA
		sequence:PIR:S11175"
		/note="unnamed protein product;
		Function: Hnml of S. cerevisiae is
		the unique coline permease in

yeast (Km of 0.5 micromolar).  
 Regulation: in *S. cerevisiae*,  
 expression of HNML gene is  
 regulated by the phospholipid  
 precursors inositol and choline  
 and this regulation involves the  
 trans-acting factors Ino2p, Ino4p  
 and Opilp. Remark: alternate name  
 for *S. cerevisiae* Hnml is YGL077c.  
 Similarity: Hnml of *S. cerevisiae*  
 belongs to the APC family, which  
 encompasses amino acid permeases  
 more related to the mammalian  
 cationic amino-acid transporter  
 family (Tea/ecoR). Title: strong  
 similarity to choline permease  
 Hnml -*Saccharomyces cerevisiae*  
 plasma membrane"

/citation=[12]  
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 /citation=[24]  
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 SGTPSKATFSDDAYELARVGKKEV  
 GGPAGLVYGFGLGVWAGIISVFISMGELASMMPSA  
 GGQYHWVSILAPRSARKFLSHVTG  
 SVCIIAWTAAPTAAYLAASVLQSTIAMNIPSYD  
 PKGWHITLIMWAILLVCTVLNTWL  
 GMILPVIEVLILLVHVLGFFAVLVPLVYLGPKEAD  
 PRSIFTVSFDYGGWGDLTATFIG  
 LKGTVAAFVGTGAVHMAEEVANSSRVVPRSMML  
 ALMINGATGFAILIAFLFTAGDLL  
 KIVESSASYPFMYMLASSTGSKGAAVVLSSMMAI  
 LQACAGLAGISSGSRMLWSFSREQ  
 AIPGWRWVRQVNQRTLVPFHSTLVVVVAAGLLSL  
 INIGSAVVLNIIILSLVLEAFFASY  
 MISLTLLLYRGGVLNWGPFRVKGLGTANNIFAI  
 AYSIIMMFFGCWPPENHPAPKNIN  
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intron	complement(5457..5492)	/locus-tag="An18g00960" /number=1
exon	complement(5493..5664)	/locus-tag="An18g00960" /number=2
intron	complement(5665..5745)	/locus-tag="An18g00960" /number=2
exon	complement(5746..6075)	/locus-tag="An18g00960" /number=3
intron	complement(6076..6139)	/locus-tag="An18g00960" /number=3
exon	complement(6140..6159)	/locus-tag="An18g00960" /number=4
intron	complement(6160..6224)	/locus-tag="An18g00960" /number=4
exon	complement(6225..6602)	/locus-tag="An18g00960" /number=5
intron	complement(6603..6673)	/locus-tag="An18g00960" /number=5
exon	complement(6674..6746)	/locus-tag="An18g00960"

intron	complement(6747..6799)	/number=6 /locus-tag="An18g00960" /number=6
exon	complement(6800..6899)	/locus-tag="An18g00960" /number=7
intron	complement(6900..7248)	/locus-tag="An18g00960" /number=7
exon	complement(7249..7379)	/locus-tag="An18g00960" /number=8
gene	complement(<7770..>8415 )	/locus-tag="An18g00970"
mRNA	complement(join(<7770.. 8282,8380..>8415))	/locus-tag="An18g00970"
CDS	complement(join(7770..8 282,8380..8415))	/locus-tag="An18g00970"
		/note="unnamed protein product; Title: weak similarity to hypothetical protein BAA96207.1 - Oryza sativa" /codon-start=1 /protein-id="CAK47174.1" /db-xref="GI:134084141" /translation="MLCTHAGGEGARSGRPDDRQ GHQPISVALWLCAPPPGFLSGRTS LASAGISNPDGATAVNTCETVGCLGLTACGQDCL SSRAALAEALLLGLCCVGDGGGRA PANPNKMDRYLLLYCRLGLTLDGPIVVVVVHTLS LSCSPPTQLHPPPLLASLHSFFPP ESLGRVPISIIYAHMRHAAAKIV"
exon	complement(7770..8282)	/locus-tag="An18g00970" /number=1
intron	complement(8283..8379)	/locus-tag="An18g00970" /number=1
exon	complement(8380..8415)	/locus-tag="An18g00970" /number=2
gene	<8621..>9700	/locus-tag="An18g00980"
mRNA	join(<8621..8764, 8830..9156,9214..9356, 9406..>9700)	/locus-tag="An18g00980"
CDS	join(8621..8764, 8830..9156,9214..9356, 9406..9700)	/locus-tag="An18g00980"
		/note="unnamed protein product; Function: M. grisea Pth11 is a pathogenicity gene. Function: M. grisea Pth11p is likely to be involved in host surface recognition. Function: M. grisea pth11 mutants of strain 4091-5-8 are nonpathogenic due to a defect in appressorium differentiation. Localization: in M. grisea, a Pth11-green fluorescent protein fusion localised to the cell membrane and vacuoles. Similarity: similarity of the predicted A. niger protein and M. grisea Pth11 is limited to the N-terminal half of the protein sequences. Title: weak similarity to integral membrane protein PTH11 - Magnaporthe grisea plasma

		membrane"
		/citation=[52]
		/codon-start=1
		/protein-id="CAK47175.1"
		/db-xref="GI:134084142"
		/translation="MTDHSAAVKVVTCTLLIVSF IAVVACLTNNWQVLRKVSSVALL LSTLIASIASGAAVSVAATHGLGQASPLTDAQVV VMQKALYSMEVLYVLTGLGLKLSV MVLFYSLLSSTGQSKSVLAATGLLLIWVVVMVIV VCLQCHPPEVWNIVGGTCLDLGI WIAFGVMNVLVEIMIIAVPSFIIIFRLKLSLKRRLL VVISCFGIRILDIAGSIVQLCYVR NFKIHADSPMPTNVWQWAICSQVLQTVAILSACV PYLREFLESFSPGMFKPTELKHPT VQSAYNATKCSDSIELMRPESTKDT"
sig-peptide	8621..8698	/locus-tag="An18g00980"
		/inference="protein"
mat-peptide	join(8699..8764, 8830..9156,9214..9356, 9406..9697)	motif:SignalP:2.0"
		/locus-tag="An18g00980"
		/product="unnamed"
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intron	8765..8829	/locus-tag="An18g00980"
		/number=1
exon	8830..9156	/locus-tag="An18g00980"
		/number=2
intron	9157..9213	/locus-tag="An18g00980"
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exon	9214..9356	/locus-tag="An18g00980"
		/number=3
intron	9357..9405	/locus-tag="An18g00980"
		/number=3
exon	9406..9700	/locus-tag="An18g00980"
		/number=4
gene	complement(<9787..>9927 )	/locus-tag="An18g00990"
mRNA	complement(<9787..>9927 )	/locus-tag="An18g00990"
CDS	complement(9787..9927)	/locus-tag="An18g00990"
		/note="unnamed protein product; Title: strong similarity to EST an-1359 -Aspergillus niger"
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		/protein-id="CAK47176.1"
		/db-xref="GI:134084143"
		/translation="MRAATLLLVALLSAVALALPT TNNVERAAADANVRQMDELTVAAI SK"
sig-peptide	complement(9877..9927)	/locus-tag="An18g00990"
		/inference="protein"
		motif:SignalP:2.0"
mat-peptide	complement(9790..9876)	/locus-tag="An18g00990"
		/product="unnamed"
exon	complement(9787..9927)	/locus-tag="An18g00990"
		/number=1
gene	<10500..>11479	/locus-tag="An18g01000"
mRNA	join(<10500..10749, 10812..11041, 11105..>11479)	/locus-tag="An18g01000"
CDS	join(10500..10749,	/locus-tag="An18g01000"

10812..11041,  
11105..11479)

		/note="unnamed protein product; Similarity: the nucleotide sequence of the ORF shows strong similarity to the ESTs an-2192 and an-2204 of <i>A. niger</i> . Title: strong similarity to EST an-2192 - <i>Aspergillus niger</i> " /codon-start=1 /protein-id="CAK47177.1" /db-xref="GI:134084144" /translation="MYSYEKVNRRDDSDQGLLAE DSERVAPQPRVSRFPSWTNALLLL GLLFSLSLNVGWVFVQKGHNVP IQDLDPDAAMAK QRSPYTGLAWDTHKPYSHHSEYTS ENATHADEMWESLSMDPMVIAPTWEWAQSKGLSD SWAFPWDSNRRIYFIKVFHQLHCL KLMRHSYHELWSGQESSIPAPHIEHCLDSL RQDL MCKADDTMPPSLQLLNGGGEGQQM QCKDFDKLVAWSKAPERNACYKRLTDYKPIVHSI ERYAFCPEDSEHYPTMSKYFEEHG HYADPFSE"
exon	10500..10749	/locus-tag="An18g01000" /number=1
intron	10750..10811	/locus-tag="An18g01000" /number=1
exon	10812..11041	/locus-tag="An18g01000" /number=2
intron	11042..11104	/locus-tag="An18g01000" /number=2
exon	11105..11479	/locus-tag="An18g01000" /number=3
gene	<11980..>13464	/locus-tag="An18g01010"
mRNA	join(<11980..12137, 12198..>13464)	/locus-tag="An18g01010"
CDS	join(11980..12137, 12198..13464)	/locus-tag="An18g01010"

/inference="profile:COGS:COG0477"  
/note="unnamed protein product;  
Function: FLU1 of *C. albicans*  
facilitates resistance to  
fluconazole and cycloheximide in  
the fluconazole-hypersensitive *S.*  
*cerevisiae* strain YKKB-13 lacking  
the ABC (ATP-binding cassette)  
transporter gene PDR5. Function:  
FLU1 of *C. albicans* facilitates  
resistance to mycophenolic acid in  
*C. albicans*. Function: FLU1 of *C.*  
*albicans* is involved in the  
resistance to azol derivatives in  
*C. albicans*. Function: MDR1 of *C.*  
*albicans* facilitates resistance to  
the anti-mitotic drug benomyl and  
to the dihydrofolate reductase  
inhibitor methotrexate.  
Similarity: N-terminus of the *A.*  
*niger* protein is app. 120 aa  
shorter than in FLU1 of *C.*  
*albicans*. Similarity: the  
predicted *A. niger* protein shows  
strong similarity to fluconazole



		resistance protein FLU1 of <i>C. albicans</i> , which is a permease belonging to the major facilitator superfamily. Title: strong similarity to fluconazole resistance protein FLU1 - <i>Candida albicans</i> /citation=[59] /codon-start=1 /protein-id="CAK47178.1" /db-xref="GI:134084145" /translation="MDEEDGHCKETEVTVQSTSP VDSADYDPFDPQTRSTTYKWITVV LVAGLSTMVQLSTIIAAPVSPSILAHFHS DNALY RTLIVSIWELGEIVAPLLWGPLSE LYGRQWPLNIANLFFVAFLAGTAASTSIQMLIAF RFLSGAATAASAIGPGIVSDFPE ESRGRAMSIMSLTGALGPVVGPIIGSYLGEKAGW RWAFLPTIATGTLSLLILVVYRE TYSVTLQKRKARQQNPESGSKSPEDTDKTASQVF FKAILRPLRLLIRSPMLILVTFYL SVVYGYTYLVMTTIAPLFQDVYGFSEGLAFL GLCLGLILGAFLCSFLLDRYVRTA RARSGTSKPEQRLPPVLIACFVMSGGLFLFGWTA QYHVQWIAPIIGTGIIIGFLVSTT ITLQTYVVDLFGIYAASATSAMLVPRNACAAFLP LAGPPLFDRLGYNWGGTLLALIVL VFSLMPLIFINYGERLRGKNLLDD"
exon	11980..12137	/locus-tag="An18g01010"
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intron	12138..12197	/locus-tag="An18g01010"
		/number=1
exon	12198..13464	/locus-tag="An18g01010"
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gene	complement(<14029..>15172)	/locus-tag="An18g01020"
mRNA	complement(join(<14029..14318,14411..14845,14917..>15172))	/locus-tag="An18g01020"
CDS	complement(join(14029..14318,14411..14845,14917..15172))	/locus-tag="An18g01020"

/EC-number="1.13.11.4"  
 /inference="profile:COGS:COG3435"  
 /inference="similar to AA  
 sequence:UniProtKB:AF173167.3"  
 /note="unnamed protein product;  
 Complex: the estimated molecular  
 mass of the purified gentisate 1,  
 2-dioxygenase of *P. alcaligenes*  
 was 154 kDa, with a subunit mass  
 of 39 kDa. its structure is  
 deduced to be a tetramer. Remark:  
 gentisate 1,2-dioxygenase of *P.*  
*alcaligenes* exhibits typical  
 saturation kinetics and has an  
 apparent Km of 92 microM for  
 gentisate. this enzyme has broad  
 substrate specificities towards  
 alkyl and halogenated gentisate  
 analogs. Similarity: the predicted  
*A. niger* protein shows strong

```

similarity to gentisate
1,2-dioxygenase of P. alcaligenes
and conserved hypothetical
proteins from other procaryotic
species. Title: strong similarity
to gentisate 1,2-dioxygenases xlnE
- Pseudomonas alcaligenes"
/citation=[50]
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MLVNPARDAPYTTDTLYAGLQLVM
PNETAPAHRHTAFAMRYIIIEGNGGFTAVHGKRIK
MQKGDVILTPTWNYHDHGKDGTP
MIWLDGLDLPNFRHFPVHFVDHYDQPRYP AEDVD
SATSPIVFPWDKMKAELDKAPGTW
AVRRYL RADGSEGGS AERVDAGTSSLPRQET TSA
VYHVIAGSGCSEIGDKTLVWETGD
TFCVPSWYKYRHIAAEGETVYLYRFDDKPMISAL
GFYRSIDTDLATLVSQ"
exon      complement(14029..14318 /locus-tag="An18g01020"
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intron    complement(14319..14410 /locus-tag="An18g01020"
)
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exon      complement(14411..14845 /locus-tag="An18g01020"
)
                                     /number=2
intron    complement(14846..14916 /locus-tag="An18g01020"
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                                     /number=2
exon      complement(14917..15172 /locus-tag="An18g01020"
)
                                     /number=3
gene      <15614..>17392           /locus-tag="An18g01030"
mRNA      join(<15614..15661,    /locus-tag="An18g01030"
15723..16281,
16347..16503,
16584..16739,
16803..16942,
17034..>17392)
CDS       join(15614..15661,    /locus-tag="An18g01030"
15723..16281,
16347..16503,
16584..16739,
16803..16942,
17034..17392)

/inference="profile:COGS:COG0654"
/inference="profile:PFAM:PF01360"
/note="unnamed protein product;
Function: Mak1 from N.
haematococca specifically
hydroxylates the phytoalexins
medicarpin and
maackiain, converting them to less
fungitoxic derivatives.
Localization: heterologous
expression of the Mak1 cDNA

```

construct in plants indicated that Mak1 protein accumulates in the plant cytoplasm, associated with endoplasmic reticulum membranes. Similarity: the predicted A. niger protein shows strong similarity to Mak1 from the fungal pathogen N. haematococca. Mak1 belongs to the flavin-containing mono-oxygenases. best matches are with putative salicylate hydroxylases of several procaryotic species. Title: strong similarity to maackiain detoxification protein 1 MAK1 - Nectria haematococca endoplasmatic reticulum"

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 TPVLGEVGAGIQIPSNSTRILFSL  
 GLQSYLEPYVTAPESISFRRWQNGKVI GLTKLIP  
 NFVNNFKAPYYVIHRADFHSALCQ  
 KALDVGVEIELGAKVVDYDPIVGSITLADGTKHS  
 ADLIVAADGIKSVARNVVLQGD  
 EM  
 RFQGGPGFAAYRAVVDVGKMRRDPDL  
 SWILEKPAL  
 NIWIGDSRHVMTYTIGAGKAFNMV  
 LSHPEMTDPGTWKPETALEDMKAEFQGWDPILSK  
 IIGMVEKTVKWPLLTGTLLQNWTV  
 GKLVIILGDAAHAMVPYMSQGAAMAVEDGIALSRS  
 LSHMTSRDQLQKALSIFQEVRKKR  
 AGHMQEASLLNGKLWHFPDGSLLQARDEAMAPEV  
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exon	15723..16281	/locus-tag="An18g01030"
		/number=2
intron	16282..16346	/locus-tag="An18g01030"
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		/number=3
intron	16504..16583	/locus-tag="An18g01030"
		/number=3
exon	16584..16739	/locus-tag="An18g01030"
		/number=4
intron	16740..16802	/locus-tag="An18g01030"
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exon	16803..16942	/locus-tag="An18g01030"
		/number=5
intron	16943..17033	/locus-tag="An18g01030"
		/number=5
exon	17034..17392	/locus-tag="An18g01030"
		/number=6
gene	<17766..>20491	/locus-tag="An18g01040"
mRNA	join(<17766..17864,	/locus-tag="An18g01040"

CDS

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18398..19163,  
19373..19935,  
20037..20252,  
20325..>20491)  
join(17766..17864,  
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18108..18343,  
18398..19163,  
19373..19935,  
20037..20252,  
20325..20491)  
  
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/inference="profile:PFAM:PF00172"  
/inference="similar to AA  
sequence:UniProtKB:ENU56097.1"  
/note="unnamed protein product;  
Phenotype: facB recessive loss of  
function mutants in A. nidulans  
are deficient in acetate induction  
of acetyl-CoA synthase, isocitrate  
lyase, malate  
synthase, acetamidase, and  
NADP-isocitrate dehydrogenase.  
Similarity: the predicted A. niger  
protein shows similarity to  
acetate regulatory DNA binding  
protein FacB (facB) from A.  
nidulans, which belongs to the  
GAL4-type zinc cluster  
transcriptional activators. Title:  
similarity to acetate regulatory  
DNA binding protein facB -  
Aspergillus nidulans"  
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DAPRKENPLSNQSERFSDFAGTEDTIDAMGAVAF  
ADEEDCGFFGPSSNIAFLRHLSCA  
VAHSASAQKEITSPPLDRVAYDGGFVSATRPSSP  
SHDQRPESLEGEKFDKFALPPPEE  
SLALIHRYFADTGLLFPYIHPPTFFETYAELKDN  
SKRVRRTWLGLLNIIILAMAKLTAV  
SGTTSAETGISESAIYYHRALSLCKGEILRGTTL  
EVGRYSIYAPVRARVPVYLRATKI  
NTVQYLLVMGQYLQGTQKSVQAWTIHGLAVKAAL  
QLGLHSGKASRAFTPLEQEVKRKT  
WFGCVVLDVRANLFLNKRKTIQQANIRVSTLYK  
QIANIIDRIYGQNLGCDSPLSIGE  
TVGRVLGIENQLFSWVLGLPESLRQVTVQSMREE  
IERSEVGDEGHHKLYPLKFRIILT  
LRYFHVQILLHRPILVKFLDATGPSGLEADEVKL  
LNDIGYSSMNKCVDSAMGIIDIIH  
ELVSTTGWQKDLLGAWWYSLYYTFNAALVIIGAM  
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exon	20325..20491	/locus-tag="An18g01040"
		/number=7
gene	complement(<20773..>225	/locus-tag="An18g01050"
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mRNA	complement(join(<20773.	/locus-tag="An18g01050"
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	21710..22119,	
	22180..22303,	
	22370..>22555))	
CDS	complement(join(20773..	/locus-tag="An18g01050"
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	21710..22119,	
	22180..22303,	
	22370..22555))	
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		/inference="profile:PFAM:PF03055"
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		Catalytic activity:
		lignostilbene-alpha,beta-dioxygena
		se isozymes (LSD-I, II, and III)
		of P. paucimobilis catalyse the
		reaction
		1,2-bis(4-hydroxy-3-methoxyphenyl)
		ethylene + O(2) = 2 vanillin
		Cofactor:
		lignostilbene-alpha,beta-dioxygena
		se isozymes (LSD-I, II, and III)
		of P. paucimobilis require iron as
		a cofactor. Complex: LSD-I, II,
		and III consist of alpha
		alpha,alpha beta, and beta beta
		subunits, respectively. they show
		different specificities for
		several substrates that are

stilbene and styrene derivatives.  
Function: LSD of *P. paucimobilis*  
catalyses the oxidative cleavage  
of the interphenyl double bond in  
the synthetic substrate and  
lignin-derived stilbenes. it is  
responsible for the degradation of  
a diarylpropane-type structure in  
lignin. Similarity: the predicted  
*A. niger* protein shows strong  
similarity to subunit lsdB of  
lignostilbene-alpha,beta-dioxygena  
se isozyme LSD-III of *P.*  
*paucimobilis* and related  
dioxygenases from several plant  
species. Title: strong similarity  
to subunit lsdB of  
lignostilbene-alpha,beta-dioxygena  
se isozyme LSD-III -*Pseudomonas*  
*paucimobilis*"  
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CDS	join(24984..25058, 25166..25301, 25564..25745, 25812..26003, 26080..26144, 26206..26646, 26722..27303, 27423..27426)	/locus-tag="An18g01070"  /inference="profile:COGS:COG0477" /note="unnamed protein product; Function: FLU1 of C. albicans facilitates resistance to fluconazole and cycloheximide in the fluconazole-hypersensitive S. cerevisiae strain YKKB-13 lacking the ABC (ATP-binding cassette) transporter gene PDR5. Function: FLU1 of C. albicans facilitates resistance to mycophenolic acid in C. albicans. Function: FLU1 of C. albicans is involved in the resistance to azol derivatives in C. albicans. Function: MDR1 of C. albicans facilitates resistance to the anti-mitotic drug benomyl and to the dihydrofolate reductase inhibitor methotrexate. Similarity: N-terminus of the A. niger protein is app. 120 aa shorter than in FLU1 of C. albicans. Similarity: the predicted A. niger protein shows strong similarity to fluconazole resistance protein FLU1 of C. albicans, which is a permease belonging to the major facilitator superfamily. Title: similarity to fluconazole resistance protein FLU1 - Candida albicans" /citation=[59] /codon-start=1 /protein-id="CAK47184.1" /db-xref="GI:134084151" /translation="MRGVEELASENKDETRSGRR NLGGKQHFRRGGERSVDLALRPPR RGTPGSPQSQLAHGVSCSSWLVPVRVRIPTDDPGD PLRWPSWLKLSVILSTSLVNFVSN MGGAGLSVAVPVLMMQLQRSQAEVTQLLTNLNLF



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                Catalytic activity:
                lysophospholipase catalyses the
                reaction 2-lysophosphatidylcholine
                + H(2)O = glycerophosphocholine +
                a fatty acid anion. Pathway:
                lysophospholipase is involved in
                phospholipid degradation.
                Similarity: the predicted A. niger
                protein shows strong similarity to
                the protein sequences
                lysophospholipase (sequence 5 and
                sequence 7) of patents
                WO0127251-A/5 and WO0127251-A/7
                from A. oryzae (AC# AX112082 and
                AC# AX112084) and to other fungal
                lysophospholipases. Title: strong
                similarity to lysophospholipase
                from patent WO0127251-A -

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CDS	complement(join(30960.. 31045,31081..31220, 31273..31630, 31702..32218))	

the function of the protein.  
 Similarity: the predicted A. niger  
 protein shows strong similarity to  
 the protein sequence alcohol  
 dehydrogenase (sequence 19) of  
 patent EP0845532-A/19 from an  
 unclassified organism (AC# A92108)  
 and to other zinc-containing  
 dehydrogenases. Title: strong  
 similarity to alcohol  
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 EP0845532-A - Unclassified  
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          system of(-)-versicolorin B.
          Pathway: versicolorin B synthase
          from A. parasiticus is involved in
          the aflatoxin biosynthetic
          pathway. Remark: a splice site was
          detected upstream of the START
          codon. Remark: aflatoxins comprise
          a group of polyketide-derived
          carcinogenic mycotoxins. Remark:
          the genes encoding the aflatoxin
          biosynthetic enzymes in A.
          parasiticus are clustered. Remark:
          versicolorin B synthase from A.
          parasiticus possesses an
          amino-terminal sequence homologous
          to the ADP-binding region of other
          flavoenzymes, but does not require
          flavin or nicotinamide cofactors
          for its cyclase activity.
          Similarity: the predicted A. niger
          protein shows strong similarity to
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		Remark: the patent does not
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		the function of the protein.
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		protein shows similarity to the
		protein fragment (SEQ ID NO:

		51484) of patent EP1033405-A2 from A. thaliana (AC# AAG41385) and to putative sterol desaturase family proteins. Title: similarity to protein fragment SEQ ID NO:51484 from patent EP1033405-A2 - Arabidopsis thaliana" /codon-start=1 /protein-id="CAK47190.1" /db-xref="GI:134084157" /translation="MSGTHPNPKDSMKSTWRRRLD RAEWTIYHWFYEILGVHPEHLDKE VPVHQKTEKIPYMRTWSQHVWILYHAFIPLAVHH VYVSYTGQNFTPVGAFFFYISIAFK LIAIHQLQVMRRMGHVLGFLDGDQHGVDGVPDVG VAKVVRSLISTSTFRPIMTVFLSY RVSQAPAQMSWGWLPLEIGLYGIILDFWFYWYHR LMHDVGSGLWKYHRTTHLTKHPNPL LTLYADTEQEFFDIAGIPLMTYFSMRLMGMPMGF YEWWICHQYVVFTELAGHSGLRMH ASPPSTLDWLLRLIGAELVIEDHDLHHRKGWKKS HNYGKQTRLWDKIFGTCHERIESR EGNVDYDNTVRMPIF" /locus-tag="An18g01130" /number=1
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CDS

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42401..>42671)  
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/inference="profile:COGS:COG0477"  
/inference="similar to AA  
sequence:UniProtKB:AF188621.1"  
/note="unnamed protein product;  
Function: FLU1 of *C. albicans*  
facilitates resistance to  
fluconazole and cycloheximide in  
the fluconazole-hypersensitive *S.*  
*cerevisiae* strain YKKB-13 lacking  
the ABC (ATP-binding cassette)  
transporter gene PDR5. Function:  
FLU1 of *C. albicans* facilitates  
resistance to mycophenolic acid in  
*C. albicans*. Function: FLU1 of *C.*  
*albicans* is involved in the  
resistance to azol derivatives in  
*C. albicans*. Function: MDR1 of *C.*  
*albicans* facilitates resistance to  
the anti-mitotic drug benomyl and  
to the dihydrofolate reductase  
inhibitor methotrexate.  
Similarity: the predicted *A. niger*  
protein shows strong similarity to  
fluconazole resistance protein  
FLU1 of *C. albicans*, which is a  
permease belonging to the major  
facilitator superfamily. Title:  
strong similarity to fluconazole  
resistance protein FLU1 - *Candida*  
*albicans*"  
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AIFSSSTTNVARVFGVGIEVATLSSSLYICGYAS  
GPLVWAPLSELKGRKPPIVVAMLG  
FGIFNTAVAVAKDLQTIMICRFFCGVFGSCPLAV  
VAAVFSIDIYNNRTRGVAIAMFSST  
VFLGPLLAPFIGGFINTSYLGWRWTAYIPAFMGY  
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ELRRRTKNWGIHAKQEEIEVDLRELLVNNFSRPL  
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PEWRLPPVIIGGALFAGGLFWFGWTGFTKSIHWI  
VPTLSGLFTGLGLLIIFIQLFNLY  
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VAEH"

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exon

40728..41152



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exon	42401..42671	/number=2 /locus-tag="An18g01150"
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		/locus-tag="An18e01160"
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		/note="codon recognized: CAC"
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 /inference="profile:PFAM:PF02877"  
 /note="unnamed protein product;  
 Catalytic activity: the NAP  
 protein of Z. mays catalyses the  
 reaction NAD(+) +  
 {ADP-D-ribosyl}(N)-acceptor <=>  
 nicotinamide +  
 {ADP-D-ribosyl}(N+1)-acceptor.  
 Function: the NAP protein of Z.  
 mays is involved in programmed  
 cell death or apoptosis.  
 Localization: the NAP protein of  
 Z. mays is a nuclear enzyme.  
 Remark: the ADP-D-ribosyl group of  
 NAD(+) is transferred to an  
 acceptor carboxyl group on a  
 histone or the enzyme itself, and  
 further ADP-ribosyl groups are  
 transferred to the 2'-position of  
 the terminal adenosine moiety,  
 building up a polymer with an  
 average chain length of 20-30  
 units. Remark: the NAP  
 polynucleotide sequences can be  
 used for modulation of programmed  
 cell death in eukaryotic cells.  
 the method is used, specifically  
 in plants, to induce, or protect  
 against, programmed cell  
 death, depending on the extent to  
 which PARP activity is reduced.

reducing expression of endogenous NAP class PARP only is also used to modulate programmed cell death, to increase growth rate and to produce plant cells that are more tolerant of stress (cold, chemical treatments, pathogens, pests, drought, heat, etc. , or during transformation). particular applications are generation of plants that are resistant to fungi or nematodes; are male or female sterile ; or have better seed-shatter properties. the methods are also used to improve growth of transformed plant cells (and derived calli or complete plants). Similarity: the predicted A. niger protein shows strong similarity to the protein sequence poly(ADP-ribose) polymerase NAP protein of patent WO200004173-A1 from Z. mays (AC# AAY68834) and from many other eucaryotic organisms. Title: strong similarity to poly(ADP-ribose) polymerase NAP protein from patent WO200004173-A1 - Zea mays nucleus"

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 TKQINVPVDDTCPLRLTFTVYIDP  
 TGLIWDATLNQTSATNNNNKFYRIQLLHRNNEFR  
 TWTWGRVGEHGQHALLGGGGLDE  
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 NYEEDTEDEDEDEDKVVAKKPTKP  
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 IPHAFGRNRPPVLNNDNLLKREIE  
 LLEALTDMEVANSIMKDARNTDTVHPLDRQFQGL  
 NMQEMTPLEHTSTEFIELANYLNQ  
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 IQNSCRLLWHGSRSTNFGGILSQ  
 GLRIAPPEAPVSGYMGKGVYFADMSTKSAGYCF  
 SWGSGNRGLLLLCDVEVGNPMYER  
 DTASFNAGQEAKAEAKIATLGRGRSIPGGWKDAG  
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intron 43853..43911

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mRNA	join(<46879..48454, 48518..>48537)	/locus-tag="An18g01180"
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/EC-number="3.5.1.11"  
 /note="unnamed protein product;  
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 amidohydrolase (PVA) from F.  
 oxysporum is used for the  
 enzymatic hydrolysis of penicillin  
 V (phenoxy-methylpenicillin) to  
 6-aminopenicillanic acid (6-APA).  
 6-APA is the active beta-lactam  
 nucleus used in the manufacture of  
 semi-synthetic penicillins.  
 Similarity: the predicted A. niger  
 protein shows strong similarity to  
 the protein sequence penicillin V  
 amidohydrolase (PVA) of patent  
 US5516679-A from F. oxysporum (AC#  
 AAW00291). Title: strong  
 similarity to penicillin V  
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 US5516679-A - Fusarium oxysporum  
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 SNPQTGAWILRPDGSINTALLLN  
 AHRSIYDMTIIIGKTLTERFYGSPPRYSYWSGCST  
 GGRQGYFAAAKYPNLF DGVLGAP  
 ALNFPRLIGYMFVPPVHMFHSAAPPQCVDFTFWK  
 AIIDECPLDGATDGLISDYNPQS  
 CPFKPETLVGHTVTCPEMGSDSPVTITAQHATLV  
 KQILQGPDLQDHPDLWTGLPPGAS  
 FRGTANTQVINGSIVRPVPPFPIIGWIKNFVYRD  
 PDYNVFDMTFDDFNTAYRLTLDGY  
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intron	48455..48517	/locus-tag="An18g01180" /number=1
exon	48518..48537	/locus-tag="An18g01180" /number=2
gene	complement(48889..48960 )	/gene="tRNA-Ala (AGC) " /locus-tag="An18e01190"
tRNA	complement(48889..48960 )	/gene="tRNA-Ala (AGC) " /locus-tag="An18e01190" /product="tRNA-Ala" /inference="profile:tRNAscan:1.4" /note="codon recognized: GCU"
gene mRNA	<49850..>51919 join(<49850..49888, 49981..50173, 50233..50362, 50419..50614, 50702..50828, 50883..51127, 51199..51470, 51538..>51919)	/locus-tag="An18g01200" /locus-tag="An18g01200"
CDS	join(49850..49888, 49981..50173, 50233..50362, 50419..50614, 50702..50828, 50883..51127, 51199..51470, 51538..51919)	/locus-tag="An18g01200"  /EC-number="1.14.-.-" /inference="profile:COGS:COG2124" /inference="profile:PFAM:PF00067" /inference="similar to AA sequence:UniProtKB:AFU81806.1" /note="unnamed protein product; Function: ord1 of A. flavus converts O-methylsterigmatocystin to aflatoxin B1. Pathway: ord1 of A. flavus catalyzes the last step of the aflatoxin biosynthetic pathway. Remark: aflatoxins comprise a group of polyketide-derived carcinogenic mycotoxins. Similarity: the predicted A. niger protein shows strong similarity to O-methylsterigmatocystin (OMST)-oxidoreductase (ord1) from A. flavus, which belongs to the CYP64 family of cytochrome P450-type monooxygenases. Title: strong similarity to O-methylsterigmatocystin oxidoreductase ord1 - Aspergillus flavus"

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52984..53309,  
53368..53720))

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Function: SRPK2 from M. musculus  
phosphorylates SF2/ASF, a member  
of SR splicing factors. Remark:  
overexpression of murine SRPK2  
causes disassembly of  
cotransfected SF2/ASF and  
endogenous SC35. SRPK family  
members may regulate the  
disassembly of the SR proteins in  
a tissue-specific manner.  
Similarity: the predicted A. niger  
protein shows similarity to SRPK2  
from M. musculus and strong  
similarity to putative  
serine/threonine protein kinases  
from several eucaryotic organisms.  
Title: similarity to  
SR-protein-specific kinase SRPK2 -  
Mus musculus nucleus"  
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GSGPLPLISDFGEARFGDVEKRDDIMPNNMYRAPEV  
VLKENWNYKVDIWNVAMVAWDIVI  
PRHMF DGRNADGIFDDR VHIAEMIALMGPPPASF  
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 mutants (dal5) that lack  
 allantoate transport have been  
 isolated. these strains also  
 exhibit a 60% loss of allantoate  
 transport capability. Regulation:  
 in *S. cerevisiae* Dal5 appears to  
 be sensitive to nitrogen  
 catabolite repression, feedback  
 inhibition, and trans-inhibition.  
 Regulation: in *S. cerevisiae*  
 allantoate uptake is constitutive.  
 Similarity: the predicted *A. niger*  
 protein shows strong similarity to  
 allantoate permease gene (DAL5)  
 from *S. cerevisiae*, which belongs  
 to the major facilitator  
 superfamily. Title: strong  
 similarity to allantoate permease  
 Dal5 - *Saccharomyces cerevisiae*"  
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 GFQHVHHGATLAGWRIMFLVIGLV  
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                                /note="unnamed protein product;
                                Function: M. grisea Pth11 is a
                                pathogenicity gene. Function: M.
                                grisea Pth11p likely is involved
                                in host surface recognition.
                                Function: M. grisea pth11 mutants
                                of strain 4091-5-8 are
                                nonpathogenic due to a defect in
                                appressorium differentiation.
                                Localization: in M. grisea, a
                                Pth11-green fluorescent protein
                                fusion localised to the cell
                                membrane and vacuoles. Similarity:
                                similarity of the predicted A.
                                niger protein and M. grisea Pth11
                                is limited to the N-terminal half
                                of the protein sequences. Title:
                                similarity to integral membrane
                                protein PTH11 - Magnaporthe grisea
                                plasma membrane"
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intron	58159..58325	/locus-tag="An18g01230"
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gene	<59070..>60560	/locus-tag="An18g01240"
mRNA	join(<59070..59441, 59521..59806, 59879..60178, 60237..60312, 60374..>60560)	/locus-tag="An18g01240"
CDS	join(59070..59441, 59521..59806, 59879..60178, 60237..60312, 60374..60560)	/locus-tag="An18g01240"
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		/inference="profile:PFAM:PF01360"
		/note="unnamed protein product; Catalytic activity: NahW of P.

stutzeri catalyzes the conversion  
 salicylate + NADH + O(2) <=>  
 catechol + NAD(+) + H(2)O + CO(2).  
 Pathway: NahW of P. stutzeri is  
 involved in the metabolization of  
 naphthalene and salicylates (lower  
 naphthalene degradation pathway).  
 Similarity: the predicted A. niger  
 protein shows similarity to  
 salicylate hydroxylase (nahW) of  
 P. stutzeri, which belongs to the  
 NADH-dependent monooxygenase  
 superfamily. Title: similarity to  
 salicylate hydroxylase nahW  
 -Pseudomonas stutzeri"  
 /citation=

<-----User Break----->

sequence:PIR:S45605"

/note="unnamed protein product;  
 Catalytic activity: alcohol + NAD+  
 = aldehyde or ketone + NADH.  
 Pathway: alcohol dehydrogenase  
 ADH-T from B. stearothermophilus  
 is involved in glycolysis /  
 gluconeogenesis; fatty acid  
 metabolism; bile acid  
 biosynthesis; tyrosine metabolism;  
 glycerolipid metabolism. Remark:  
 the protein sequence of alcohol  
 dehydrogenase ADH-T from B.  
 stearothermophilus NCA1503 is  
 covered by patent JP04218378-A  
 (AC# AAR26874). Similarity: the  
 predicted A. niger protein shows  
 strong similarity to thermostable  
 alcohol dehydrogenase ADH-T from  
 B. stearothermophilus NCA1503,  
 which belongs to the zinc alcohol  
 dehydrogenase (ADH) family. Title:  
 strong similarity to thermostable  
 alcohol dehydrogenase adhT -  
 Bacillus stearothermophilus"  
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 FGFIRRVCGRCDNCISGCDHHCRE  
 KRAYGQHDFDVGSFSGHTVWDADAVYPIPEGYDS  
 AHAAPLLCAGASVWACL TNNGIRP  
 SDRVGMGIGGLGHLAIKLARALRYNVVALSSSE  
 KKREEALEFGASEFYRFPNTQTPN  
 HIKPVKHL LCGSSD VDYASWVSHLPSKQNAIDH  
 ANIYRSLDLVD TNGTIYHISVTL  
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exon

complement(100363..1011  
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mRNA	join(<101875..101958, 102203..102219, 102259..102360, 102392..102399, 102621..103153, 103205..>104542)	/locus-tag="An18g01440"
CDS	join(101875..101958, 102203..102219, 102259..102360, 102392..102399, 102621..103153, 103205..104542)	/locus-tag="An18g01440"
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intron	102220..102258	/locus-tag="An18g01440"
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intron	102361..102391	/locus-tag="An18g01440"
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		/note="unnamed protein product; Function: ordA of A. parasiticus is involved in the aflatoxin biosynthesis and converts O-methylsterigmatocystin (OMST) to aflatoxins B1 or G1 and converts dihydro-O-methylsterigmatocystin (DHOMST) to aflatoxins B2 or G2. Remark: aflatoxins comprise a group of polyketide-derived carcinogenic mycotoxins. Remark: it is assumed that the ORF is N-terminally shorter and has another start codon 5' to the predicted one ; the ORF is around 400 amino acids shorter than most of the homologues cytochrome p450 proteins. Remark: ordA of A. parasiticus is also called cytochrome p450 64, cyp64 or omst oxidoreductase. Similarity: the ORF shows similarity to several cytochrome P450 related proteins from different species. Title: strong similarity to O-methylsterigmatocystin oxidoreductase ordA - Aspergillus parasiticus"
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		/number=1
exon	106647..106803	/locus-tag="An18g01450"
		/number=2
gene	<107279..>108340	/locus-tag="An18g01460"
mRNA	join(<107279..107327, 107380..107740, 107795..107907, 107966..107988, 108045..108097, 108151..>108340)	/locus-tag="An18g01460"
CDS	join(107279..107327, 107380..107740, 107795..107907, 107966..107988, 108045..108097, 108151..108340)	/locus-tag="An18g01460"
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		/note="unnamed protein product; Catalytic activity: cyclohexanol dehydrogenases convert cyclohexanol + NAD(+) <=> cyclohexanone + NADH. Function: chnA of A. sp. is an alcohol dehydrogenases proposed to catalyze the conversion of cyclohexanol to cyclohexanone (EC 1. 1. 1. 245). Phenotype: cyclohexanol was detected as the major intermediate accumulated in the chnA mutant of A. sp. Remark: chnA of A. sp. is encoded in the gene cluster for cyclohexanol oxidation. Similarity: the ORF shows similarity to several dehydrogenases from different species and with various specificities. Title: strong similarity to cyclohexanol dehydrogenase chnA - Acinetobacter sp"
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		/inference="protein motif:SignalP:2.0"
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intron	107741..107794	/locus-tag="An18g01460" /number=2
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intron	107908..107965	/locus-tag="An18g01460" /number=3
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intron	107989..108044	/locus-tag="An18g01460" /number=4
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exon	108151..108340	/locus-tag="An18g01460" /number=6
gene	<108826..>111209	/locus-tag="An18g01470"
mRNA	join(<108826..108944, 109020..109023, 109089..109305, 109377..109778, 109841..109905, 110160..110181, 110244..110293, 110355..110492, 110524..110752, 110866..110960, 111135..>111209)	/locus-tag="An18g01470"
CDS	join(108826..108944, 109020..109023, 109089..109305, 109377..109778, 109841..109905, 110160..110181, 110244..110293, 110355..110492, 110524..110752, 110866..110960, 111135..111209)	/locus-tag="An18g01470"
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involved in aflatoxin biosynthesis. Similarity: the ORF shows similarity to monooxygenases from several species and with different functions. Title: strong similarity to monooxygenase moxY -Aspergillus parasiticus" /citation=[55] /codon-start=1 /protein-id="CAK47220.1" /db-xref="GI:134084187" /translation="MANEQTCSPSINLNTHENMC KGRIQQRRYPATCNMLKKPRCVPHTQIELCTVLFASFNMISASTTDTFTQVIIIGAGM SGLAMACQLKKQLCCEDFVIYDRA PSFGGTWYFNKCCGVDIPAAFYSFSFALYPQFTC FFPKQEEILQYIHGVADEFSVALK LVGHTEWEGADWQDSEQCWEVRLREIPSGRKFT RCRILISAVGGLTNPKHVMLQGIE RFQGNIVHTALWDQETAVAGKNVIVIGNGASATQ FIPAIADDAASINQFIRHVRKCAP EEQYWSLLTPEYSIGCKRRVFDNDGYLKCLHRPN VDIITNDPVVAVEEQSITTQSGKRF PADLIADVLDYGRCLRLGSLSRSTMSTGEVVMG VRDKNIGTVSAAYKHLRRWPWRNF LTFSTFSDPFLAGAIHQLSIQLKVSVVIKQASEE RFNTKLKSALRKTVFTNMCRSLPA STISLVRVLTIVVEEKPSLSLL" /locus-tag="An18g01470" /number=1

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intron 109779..109840 /locus-tag="An18g01470" /number=4

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exon 109841..109905

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		Function: eln2 of C. cinereus
		encodes a novel type of microsomal
		cytochrome P450 enzyme, with is
		involved in mushroom
		morphogenesis. Phenotype: a
		dominant mutation of the
		elongationless2 (eln2) gene of the
		mushroom C. cinereus affects
		pattern formation in the
		development of fruit body
		primordia, causing dumpy primordia
		which culminate in mature fruit
		bodies with short stipes.
		Similarity: the ORF shows
		similarity to several cytochrome
		p450 related proteins from
		different species, which have
		different cellular functions.
		Title: strong similarity to
		cytochrome p450 related protein
		eln2 - Coprinus cinereus"
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		TLPWRVFDQWSKTYGPIMSAQFGRQTLILITSPT
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		ITKGLHMLIRQYDDWLRHLHQRLDAPLLSPRASNT
		YHPIQDLESKQLMFDLLRSNDFDA
		HFERYSGSLMFALAYGFRLLSPKGQELRDMRTIQ
		GNFTYAARVGTWIVDAIPVLNLYLP
		AVVAPWKRLAEKLFKLEASVHTRHLEKGLNSEPW
		NWSKEFAASKHAEGMPRLDLAYNL
		GILVDAGFETTWTVMKIFVLAMRSDPRFVAVARK
		ELDEVVGEDRMPTFEDQEKLVIYIQ
		AVVDETLRWRSMA PGGIPHAARKEDTYMGYRIPK
		GATVIPLFWSMCLTDEPWDDPLEF
		RPERWFEATEKEEGRFRNFFGYGRRIC TGRHIAR
		NSLFLLMARILWAFDIQAPLGDDG
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CDS	complement(join(113565..114153,	/locus-tag="An18g01490"
	114210..114733))	
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		/inference="profile:PFAM:PF01544"
		/inference="similar to AA
		sequence:UniProtKB:SC41293.1"
		/note="unnamed protein product;
		Function: alr2 of S. cerevisiae is
		an uptake transporter for
		inorganic cations, e. g.
		magnesium, which presence seems to
		be important for resistance to the
		toxic effect of aluminum. Remark:
		alr2 of S. cerevisiae is also
		called YFL050C. Similarity: the
		predicted ORF is 395 amino acids
		shorter at the N-terminus and 57
		amino acids shorter at its
		C-terminal end than alr2 of S.
		cerevisiae (nearly the same is
		true for alr1 of S. cerevisiae).
		Title: strong similarity to ion
		transporter Alr2 -Saccharomyces
		cerevisiae plasma membrane"
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		GVLSFSFDPSLHTSHVRQRIEHS
		SHLLLTSDWICYALIDDIVDGFAPFISRVENGVV
		TVEDSVSITRPDDMGLALQRIFKL
		RKEVMNIRQPLHDKIDVIRSFARHCDISDTSSSQ
		VALYLSDICDHVVTMIANLEQAEQ
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CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
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SEA LACTOBACILLUS REUTERI AND TOXIN(P)BIND? AND CD4+ CELL? AND
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SEA LACTOBACILLUS REUTERI AND TOXIN(P)BIND? AND CD4+ CELLS
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SEA LACTOBACILLUS REUTERI AND TOXIN(P)BIND?
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0* FILE CEABA-VTB
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2* FILE FROSTI
0* FILE FSTA
5 FILE GENBANK
1 FILE IFIPAT
0* FILE KOSMET
0* FILE NTIS
0* FILE NUTRACEUT
1* FILE PASCAL
0* FILE PHARMAML
1 FILE SCISEARCH
1 FILE TOXCENTER
21 FILE USPATFULL
3 FILE USPAT2
0* FILE WATER
2 FILE WPIDS
2 FILE WPINDEX
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L1 QUE LACTOBACILLUS REUTERI AND TOXIN(P) BIND?
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L2 38 S L1
L3 34 DUP REM L2 (4 DUPLICATES REMOVED)
L4 27 S L3 AND (TABLET OR FOOD OR DIETARY SUPPLEMENT OR CONFECTIONERY)
L5 27 DUP REM L4 (0 DUPLICATES REMOVED)
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=> d 15 1
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L5 ANSWER 1 OF 27 USPATFULL on STN
AN 2007:296111 USPATFULL
TI Lactobacillus acidophillus nucleic acid sequences encoding cell surface
```

protein homologues and uses therefore

IN Klaenhammer, Todd R., Raleigh, NC, UNITED STATES  
 Altermann, Eric, Palmerston North, NEW ZEALAND  
 Buck, B. Logan, Banner Elk, NC, UNITED STATES  
 Russell, W. Michael, Newburgh, IN, UNITED STATES

PA North Carolina State University, Raleigh, NC, UNITED STATES (U.S. corporation)

PI US 20070258955 A1 20071108  
 AI US 2007-701335 A1 20070201 (11)

RLI Division of Ser. No. US 2004-831070, filed on 23 Apr 2004, PENDING

PRAI US 2003-465621P 20030425 (60)

DT Utility

FS APPLICATION

LN.CNT 5104

INCL INCLM: 424/093.400  
 INCLS: 435/252.100; 435/252.900; 435/320.100; 435/006.000; 435/007.100;  
 435/070.100; 514/002.000; 530/300.000; 530/387.100; 536/023.100

NCL NCLM: 424/093.400  
 NCLS: 435/006.000; 435/007.100; 435/070.100; 435/252.100; 435/252.900;  
 435/320.100; 514/002.000; 530/300.000; 530/387.100; 536/023.100

IC IPCI A61K0035-00 [I,A]; A61K0038-00 [I,A]; A61P0001-00 [I,A];  
 C07H0021-02 [I,A]; C07H0021-00 [I,C\*]; C07K0016-00 [I,A];  
 C07K0004-00 [I,A]; C12N0001-20 [I,A]; C12N0015-00 [I,A];  
 C12P0021-04 [I,A]; C12Q0001-68 [I,A]

IPCR A61K0035-00 [I,C]; A61K0035-00 [I,A]; A61K0038-00 [I,C];  
 A61K0038-00 [I,A]; A61P0001-00 [I,C]; A61P0001-00 [I,A];  
 C07H0021-00 [I,C]; C07H0021-02 [I,A]; C07H0021-04 [I,A];  
 C07K0004-00 [I,C]; C07K0004-00 [I,A]; C07K0014-195 [I,C\*];  
 C07K0014-335 [I,A]; C07K0016-00 [I,C]; C07K0016-00 [I,A];  
 C12N0001-20 [I,C]; C12N0001-20 [I,A]; C12N0001-21 [I,C\*];  
 C12N0001-21 [I,A]; C12N0009-00 [I,C\*]; C12N0009-00 [I,A];  
 C12N0015-00 [I,C]; C12N0015-00 [I,A]; C12P0021-04 [I,C];  
 C12P0021-04 [I,A]; C12P0021-06 [I,C\*]; C12P0021-06 [I,A];  
 C12Q0001-68 [I,C]; C12Q0001-68 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 2

L5 ANSWER 2 OF 27 USPATFULL on STN

AN 2007:197155 USPATFULL

TI Lactobacillus acidophilus nucleic acid sequences encoding cell surface protein homologues and uses therefore

IN Klaenhammer, Todd R., Raleigh, NC, UNITED STATES  
 Altermann, Eric, Palmerston North, NEW ZEALAND  
 Buck, B. Logan, Banner Elk, NC, UNITED STATES  
 Russell, W. Michael, Newburgh, IN, UNITED STATES

PA North Carolina State University, Raleigh, NC, UNITED STATES, 27695-8210 (U.S. corporation)

PI US 20070172495 A1 20070726  
 AI US 2007-701319 A1 20070201 (11)

RLI Division of Ser. No. US 2004-831070, filed on 23 Apr 2004, PENDING

PRAI US 2003-465621P 20030425 (60)

DT Utility

FS APPLICATION

LN.CNT 5104

INCL INCLM: 424/234.100  
 INCLS: 514/044.000; 435/006.000; 435/007.320; 435/069.100; 435/252.900;  
 435/471.000; 530/350.000; 536/023.700

NCL NCLM: 424/234.100  
 NCLS: 435/006.000; 435/007.320; 435/069.100; 435/252.900; 435/471.000;  
 514/044.000; 530/350.000; 536/023.700

IC IPCI A61K0048-00 [I,A]; A61K0039-02 [I,A]; C12Q0001-68 [I,A];  
G01N0033-554 [I,A]; C07H0021-04 [I,A]; C07H0021-00 [I,C\*];  
C12P0021-06 [I,A]; C07K0014-335 [I,A]; C07K0014-195 [I,C\*];  
IPCR A61K0048-00 [I,C]; A61K0048-00 [I,A]; A61K0039-02 [I,C];  
A61K0039-02 [I,A]; C07H0021-00 [I,C]; C07H0021-04 [I,A];  
C07K0014-195 [I,C]; C07K0014-335 [I,A]; C12N0001-21 [I,C\*];  
C12N0001-21 [I,A]; C12N0009-00 [I,C\*]; C12N0009-00 [I,A];  
C12P0021-06 [I,C]; C12P0021-06 [I,A]; C12Q0001-68 [I,C];  
C12Q0001-68 [I,A]; G01N0033-554 [I,C]; G01N0033-554 [I,A]  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 3

L5 ANSWER 3 OF 27 USPATFULL on STN  
AN 2007:140436 USPATFULL  
TI Delivery of trefoil peptides  
IN Hans, Wolfgang Christian, Landshut, GERMANY, FEDERAL REPUBLIC OF  
Steidler, Lothar, Lokeren, BELGIUM  
Remaut, Erik Rene, Lovendegem, BELGIUM  
PI US 20070122427 A1 20070531  
AI US 2007-654879 A1 20070118 (11)  
RLI Division of Ser. No. US 2002-30390, filed on 16 Apr 2002, PENDING A 371  
of International Ser. No. WO 2000-EP6343, filed on 5 Jul 2000  
PRAI EP 1999-870143 19990705  
DT Utility  
FS APPLICATION  
LN.CNT 1335  
INCL INCLM: 424/200.100  
INCLS: 435/252.300; 435/252.900  
NCL NCLM: 424/200.100  
NCLS: 435/252.300; 435/252.900  
IC IPCI A61K0039-02 [I,A]; C12N0001-21 [I,A]  
IPCR A61K0039-02 [I,C]; A61K0039-02 [I,A]; C12N0001-21 [I,C];  
C12N0001-21 [I,A]  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 4

L5 ANSWER 4 OF 27 USPATFULL on STN  
AN 2007:134502 USPATFULL  
TI Corynebacterium glutamicum genes encoding metabolic pathway proteins  
IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF  
Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF  
Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF  
Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF  
Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF  
PA BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF  
(non-U.S. corporation)  
PI US 20070117183 A1 20070524  
AI US 2006-511140 A1 20060828 (11)  
RLI Division of Ser. No. US 2005-55822, filed on 11 Feb 2005, PENDING  
Continuation of Ser. No. US 2000-606740, filed on 23 Jun 2000, ABANDONED  
PRAI DE 1999-19932125 19990709  
DE 1999-19932227 19990709  
DE 1999-19932228 19990709  
DE 1999-19932230 19990709  
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DE 1999-19933006 19990714  
DE 1999-19940764 19990827  
DE 1999-19940766 19990827

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DE	1999-19932186	19990709
DE	1999-19932922	19990714
DE	1999-19932926	19990714
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DE	1999-19940765	19990827
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DE	1999-19941394	19990831
DE	1999-19942076	19990903
DE	1999-19942086	19990903
DE	1999-19942095	19990903
DE	1999-19942129	19990903
US	1999-141031P	19990625 (60)
US	1999-142101P	19990702 (60)
US	1999-148613P	19990812 (60)
US	2000-187970P	20000309 (60)

DT Utility  
FS APPLICATION

LN.CNT 8386

INCL INCL: 435/069.100  
INCLS: 435/106.000; 435/115.000; 435/193.000; 435/252.300; 435/471.000;  
536/023.200

NCL NCLM: 435/069.100  
NCLS: 435/106.000; 435/115.000; 435/193.000; 435/252.300; 435/471.000;  
536/023.200

IC IPCI C07H0021-04 [I,A]; C07H0021-00 [I,C\*]; C12P0021-06 [I,A];  
C12P0013-04 [I,A]; C12P0013-08 [I,A]; C12P0013-00 [I,C\*];  
C12N0009-10 [I,A]; C12N0015-74 [I,A]; C12N0001-21 [I,A]

IPCR C07H0021-00 [I,C]; C07H0021-04 [I,A]; C12N0001-21 [I,C];  
C12N0001-21 [I,A]; C12N0009-10 [I,C]; C12N0009-10 [I,A];  
C12N0015-74 [I,C]; C12N0015-74 [I,A]; C12P0013-00 [I,C];  
C12P0013-04 [I,A]; C12P0013-08 [I,A]; C12P0021-06 [I,C];  
C12P0021-06 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 6

L5 ANSWER 6 OF 27 USPATFULL on STN  
AN 2007:130427 USPATFULL  
TI Delivery of trefoil peptides  
IN Hans, Wolfgang Christian, Landshut, GERMANY, FEDERAL REPUBLIC OF  
Steidler, Lothar, Lokeren, BELGIUM  
Remaut, Erik Rene, Lonendegem, BELGIUM  
PA Vlaams Interuniversitair Instituut voor Biotechnologie, BELGIUM  
(non-U.S. corporation)  
PI US 7220418 B1 20070522  
WO 2001002570 20010111  
AI US 2000-30390 20000705 (10)  
WO 2000-EP6343 20000705  
20020416 PCT 371 date  
PRAI EP 1999-870143 19990705  
DT Utility  
FS GRANTED  
LN.CNT 1334  
INCL INCLM: 424/200.100  
INCLS: 424/093.450; 424/093.200; 424/234.100; 424/192.100; 514/925.000  
NCL NCLM: 424/200.100  
NCLS: 424/093.200; 424/093.450; 424/192.100; 424/234.100; 514/925.000  
IC IPCI A01N0063-00 [I,A]; A61K0039-02 [I,A]; A61K0039-00 [I,A]  
IPCR A01N0063-00 [I,C]; A01N0063-00 [I,A]; C12N0015-09 [I,C\*];  
C12N0015-09 [I,A]; A61K0035-66 [I,C\*]; A61K0035-74 [I,A];  
A61K0038-00 [I,C\*]; A61K0038-00 [I,A]; A61K0039-00 [I,C];  
A61K0039-00 [I,A]; A61K0039-02 [I,C]; A61K0039-02 [I,A];  
A61K0048-00 [I,C\*]; A61K0048-00 [I,A]; A61P0001-00 [I,C\*];  
A61P0001-04 [I,A]; C07K0014-435 [I,C\*]; C07K0014-575 [I,A];  
C12N0001-21 [I,C\*]; C12N0001-21 [I,A]; C12N0015-16 [I,C\*];  
C12N0015-16 [I,A]; C12N0015-74 [I,C\*]; C12N0015-74 [I,A];  
C12R0001-01 [N,A]  
EXF 424/200.1; 424/192.1; 424/184.1; 424/234.1; 424/244.1; 424/246.1;  
424/93.2; 424/93.45; 514/2; 514/925; 435/69.3; 435/69.1; 435/71.1;  
435/252.9

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 7

L5 ANSWER 7 OF 27 IFIPAT COPYRIGHT 2008 IFI on STN  
AN 11053905 IFIPAT;IFIUDB;IFICDB  
TI METHOD OF IMPROVING IMMUNE FUNCTION IN MAMALS USING LACTOBACILLUS  
REUTERI STRAINS  
IN Kang Ho-Jin (KR); Kwon Ik-boo (KR); Lee Dong-Seog (KR); Mollstam Bo (SE)  
PA Unassigned Or Assigned To Individual (68000)  
PI US 2006002907 A1 20060105  
AI US 2002-531651 20021018  
WO 2002-SE1903 20021018  
20050415 PCT 371 date  
20050415 PCT 102(e) date  
FI US 2006002907 20060105  
DT Utility; Patent Application - First Publication

FS      CHEMICAL  
         APPLICATION  
ED      Entered STN: 9 Jan 2006  
         Last Updated on STN: 9 Jan 2006  
CLMN    9  
GI      1 Figure(s).  
FIG. 1. Confirmation of inhibitory ability against the binding of vero  
cytotoxin(VT) and Gb3 receptor in a culture supernatant of L. reuteri  
through competitive ELISA. Each reacted as follows, on plates coated with  
Gb3, followed by performing ELISA using mAb against VT.

=> d 15 8

L5      ANSWER 8 OF 27    USPATFULL on STN  
AN      2006:274450    USPATFULL  
TI      Gene products differentially expressed in cancerous cells  
IN      Scott, Elizabeth M., Emeryville, CA, UNITED STATES  
         Lamson, George, Emeryville, CA, UNITED STATES  
         Kassam, Altaf, Emeryville, CA, UNITED STATES  
         Zhang, Guozhong, Emeryville, CA, UNITED STATES  
         Sakamoto, Doreen, Emeryville, CA, UNITED STATES  
         Garcia, Pablo Dominguez, Emeryville, CA, UNITED STATES  
         May, Theresa, Emeryville, CA, UNITED STATES  
         Kennedy, Giulia C., Emeryville, CA, UNITED STATES  
         Kang, Sanmao, Emeryville, CA, UNITED STATES  
         Reinhard, Christoph, Emeryville, CA, UNITED STATES  
         Jefferson, Ann Bennett, Emeryville, CA, UNITED STATES  
PA      Chiron Corporation (U.S. corporation)  
PI      US 20060234246      A1    20061019  
AI      US 2004-934842      A1    20040902 (10)  
RLI      Continuation-in-part of Ser. No. US 2002-165835, filed on 6 Jun 2002,  
         ABANDONED Continuation of Ser. No. US 2000-490818, filed on 25 Jan 2000,  
         GRANTED, Pat. No. US 6429302 Continuation-in-part of Ser. No. US  
         2001-883152, filed on 15 Jun 2001, ABANDONED Continuation-in-part of  
         Ser. No. WO 2003-US15465, filed on 16 May 2003, PENDING  
PRAI    US 1999-118302P      19990202 (60)  
         US 2000-211835P      20000615 (60)  
         US 2003-445222P      20030204 (60)  
         US 2002-381533P      20020517 (60)  
DT      Utility  
FS      APPLICATION  
LN.CNT 17024  
INCL    INCLM: 435/006.000  
         INCLS: 435/007.230; 435/069.100; 435/320.100; 435/325.000; 530/350.000;  
         530/388.800; 536/023.500  
NCL    NCLM: 435/006.000  
         NCLS: 435/007.230; 435/069.100; 435/320.100; 435/325.000; 530/350.000;  
         530/388.800; 536/023.500  
IC      IPCI    C12Q0001-68 [I,A]; G01N0033-574 [I,A]; C07H0021-04 [I,A];  
         C07H0021-00 [I,C\*]; C12P0021-06 [I,A]; C07K0014-82 [I,A];  
         C07K0016-30 [I,A]; C07K0016-18 [I,C\*]  
         IPCR    C12Q0001-68 [I,C]; C12Q0001-68 [I,A]; C07H0021-00 [I,C];  
         C07H0021-04 [I,A]; C07K0014-82 [I,C]; C07K0014-82 [I,A];  
         C07K0016-18 [I,C]; C07K0016-30 [I,A]; C12P0021-06 [I,C];  
         C12P0021-06 [I,A]; G01N0033-574 [I,C]; G01N0033-574 [I,A]  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 9

L5      ANSWER 9 OF 27    USPATFULL on STN

AN 2006:98984 USPATFULL  
 TI Corynebacterium glutamicum genes encoding metabolic pathway proteins  
 IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF  
 Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF  
 Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF  
 Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF  
 Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF  
 PA BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF  
 (non-U.S. corporation)  
 PI US 20060084152 A1 20060420  
 AI US 2005-239674 A1 20050928 (11)  
 RLI Continuation of Ser. No. US 2000-746660, filed on 22 Dec 2000, ABANDONED  
 Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,  
 ABANDONED Continuation-in-part of Ser. No. US 2000-603124, filed on 23  
 Jun 2000, ABANDONED  
 PRAI DE 1999-19932125 19990709  
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US	1999-141031P	19990625 (60)
US	1999-142101P	19990702 (60)
US	1999-148613P	19990812 (60)
US	2000-187970P	20000309 (60)
US	1999-141031P	19990625 (60)
US	1999-143694P	19990714 (60)
US	1999-151778P	19990831 (60)
DT	Utility	
FS	APPLICATION	
LN.CNT	14822	
INCL	INCLM: 435/113.000	
	INCLS: 435/115.000; 435/252.300	
NCL	NCLM: 435/113.000	
	NCLS: 435/115.000; 435/252.300	
IC	IPCI C12P0013-12 [I,A]; C12P0013-08 [I,A]; C12P0013-00 [I,C*];	
	C12N0001-20 [I,A]	
	IPCR C12P0013-00 [I,C]; C12P0013-12 [I,A]; C12N0001-20 [I,C];	
	C12N0001-20 [I,A]; C12P0013-08 [I,A]	
CAS INDEXING IS AVAILABLE FOR THIS PATENT.		

=> d 15 9

L5 ANSWER 9 OF 27 USPATFULL on STN

AN 2006:98984 USPATFULL

TI Corynebacterium glutamicum genes encoding metabolic pathway proteins

IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF  
 Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF  
 Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF  
 Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF  
 Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF

PA BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF  
 (non-U.S. corporation)

PI US 20060084152 A1 20060420

AI US 2005-239674 A1 20050928 (11)

RLI Continuation of Ser. No. US 2000-746660, filed on 22 Dec 2000, ABANDONED  
 Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,  
 ABANDONED Continuation-in-part of Ser. No. US 2000-603124, filed on 23  
 Jun 2000, ABANDONED

PRAI DE 1999-19932125 19990709  
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 DE 1999-19932228 19990709  
 DE 1999-19932230 19990709  
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DE 1999-19941394	19990831
DE 1999-19942076	19990903
DE 1999-19942086	19990903
DE 1999-19942095	19990903
DE 1999-19942129	19990903
DE 1999-19932124	19990709
DE 1999-19932127	19990709
DE 1999-19932133	19990709
DE 1999-19932207	19990709
DE 1999-19932208	19990709
DE 1999-19932225	19990709
DE 1999-19932914	19990709
DE 1999-19940768	19990827
DE 1999-19940831	19990827
DE 1999-19941385	19990831
US 1999-141031P	19990625 (60)
US 1999-142101P	19990702 (60)
US 1999-148613P	19990812 (60)
US 2000-187970P	20000309 (60)

US 1999-141031P 19990625 (60)  
 US 1999-143694P 19990714 (60)  
 US 1999-151778P 19990831 (60)  
 DT Utility  
 FS APPLICATION  
 LN.CNT 14822  
 INCL INCLM: 435/113.000  
 INCLS: 435/115.000; 435/252.300  
 NCL NCLM: 435/113.000  
 NCLS: 435/115.000; 435/252.300  
 IC IPCI C12P0013-12 [I,A]; C12P0013-08 [I,A]; C12P0013-00 [I,C\*];  
 C12N0001-20 [I,A]  
 IPCR C12P0013-00 [I,C]; C12P0013-12 [I,A]; C12N0001-20 [I,C];  
 C12N0001-20 [I,A]; C12P0013-08 [I,A]  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 10

L5 ANSWER 10 OF 27 USPATFULL on STN  
 AN 2006:211028 USPATFULL  
 TI Nucleic acid sequences relating to Bacteroides fragilis for diagnostics  
 and therapeutics  
 IN Breton, Gary L., Marlboro, MA, UNITED STATES  
 PA Oscient Pharmaceuticals Corporation, Waltham, MA, UNITED STATES (U.S.  
 corporation)  
 PI US 7090973 B1 20060815  
 AI US 2000-540209 20000404 (9)  
 PRAI US 1999-128705P 19990409 (60)  
 DT Utility  
 FS GRANTED  
 LN.CNT 38850  
 INCL INCLM: 435/006.000  
 INCLS: 435/091.200; 536/023.500; 536/024.310; 536/024.330  
 NCL NCLM: 435/006.000  
 NCLS: 435/091.200; 536/023.500; 536/024.310; 536/024.330  
 IC IPCI C12Q0001-68 [I,A]; C12P0019-34 [I,A]; C12P0019-00 [I,C\*];  
 C07H0021-02 [I,A]; C07H0021-04 [I,A]; C07H0021-00 [I,C\*]  
 EXF 435/91.1; 435/91.2; 435/6; 435/320.1; 435/325; 435/352.3; 536/23.1;  
 536/24.1; 536/23.7; 536/24.32; 536/24.3; 514/44  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 11-15

L5 ANSWER 11 OF 27 USPATFULL on STN  
 AN 2006:146715 USPATFULL  
 TI Nucleic acid and amino acid sequences relating to Staphylococcus  
 epidermidis for diagnostics and therapeutics  
 IN Doucette-Stamm, Lynn, Framingham, MA, UNITED STATES  
 Bush, David, Somerville, MA, UNITED STATES  
 PA Wyeth, Madison, NJ, UNITED STATES (U.S. corporation)  
 PI US 7060458 B1 20060613  
 AI US 1999-450969 19991129 (9)  
 RLI Continuation-in-part of Ser. No. US 1998-134001, filed on 13 Aug 1998,  
 Pat. No. US 6380370, issued on 30 Apr 2002  
 PRAI US 1997-64964P 19971108 (60)  
 US 1997-55779P 19970814 (60)  
 DT Utility  
 FS GRANTED  
 LN.CNT 35708  
 INCL INCLM: 435/069.100

INCLS: 435/252.300; 435/320.100; 435/325.000; 536/023.700; 536/024.320  
NCL NCLM: 435/069.100  
NCLS: 435/252.300; 435/320.100; 435/325.000; 536/023.700; 536/024.320  
IC IPCI C07H0021-04 [I,A]; C07H0021-00 [I,C\*]  
IPCR C07H0021-00 [I,C]; C07H0021-04 [I,A]; C12N0001-21 [I,C\*];  
C12N0001-21 [I,A]; C12Q0001-68 [I,C\*]; C12Q0001-68 [I,A]  
EXF 435/6; 435/91.2; 435/69.1; 536/22.1; 536/23.1; 536/24.3  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 12 OF 27 USPATFULL on STN  
AN 2005:299042 USPATFULL  
TI Corynebacterium glutamicum genes encoding metabolic pathway proteins  
IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF  
Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF  
Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF  
Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF  
Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF  
PA BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF  
(non-U.S. corporation)  
PI US 20050260707 A1 20051124  
AI US 2005-55822 A1 20050211 (11)  
RLI Continuation of Ser. No. US 2000-606740, filed on 23 Jun 2000, ABANDONED  
PRAI DE 1999-19932125 19990709  
DE 1999-19932227 19990709  
DE 1999-19932228 19990709  
DE 1999-19932230 19990709  
DE 1999-19933005 19990714  
DE 1999-19933006 19990714  
DE 1999-19940764 19990827  
DE 1999-19940766 19990827  
DE 1999-19940832 19990827  
DE 1999-19941378 19990831  
DE 1999-19941379 19990831  
DE 1999-19942077 19990903  
DE 1999-19942079 19990903  
DE 1999-19931418 19990708  
DE 1999-19932126 19990709  
DE 1999-19932229 19990709  
DE 1999-19941396 19990831  
DE 1999-19942087 19990903  
DE 1999-19930476 19990701  
DE 1999-19931419 19990708  
DE 1999-19931420 19990708  
DE 1999-19932206 19990709  
DE 1999-19942088 19990903  
DE 1999-19942124 19990903  
DE 1999-19932928 19990714  
DE 1999-19931415 19990708  
DE 1999-19931424 19990708  
DE 1999-19931428 19990708  
DE 1999-19931434 19990708  
DE 1999-19931435 19990708  
DE 1999-19931443 19990708  
DE 1999-19931453 19990708  
DE 1999-19931457 19990708  
DE 1999-19931465 19990708  
DE 1999-19931478 19990708  
DE 1999-19931510 19990708  
DE 1999-109931541 19990708  
DE 1999-19931573 19990708  
DE 1999-19931592 19990708  
DE 1999-19931632 19990708

DE 1999-19931634 19990708  
 DE 1999-19931636 19990708  
 DE 1999-19932130 19990708  
 DE 1999-19932186 19990709  
 DE 1999-19932922 19990714  
 DE 1999-19932926 19990714  
 DE 1999-19933004 19990714  
 DE 1999-19940765 19990827  
 DE 1999-19941380 19990831  
 DE 1999-19941394 19990831  
 DE 1999-19942076 19990903  
 DE 1999-19942086 19990903  
 DE 1999-19942095 19990903  
 DE 1999-19942129 19990903  
 US 1999-141031P 19990625 (60)  
 US 1999-142101P 19990702 (60)  
 US 1999-148613P 19990812 (60)  
 US 2000-187970P 20000309 (60)  
 DT Utility  
 FS APPLICATION  
 LN.CNT 8777  
 INCL INCLM: 435/069.100  
 INCLS: 435/106.000; 435/193.000; 435/252.300; 435/471.000; 536/023.200  
 NCL NCLM: 435/069.100  
 NCLS: 435/106.000; 435/193.000; 435/252.300; 435/471.000; 536/023.200  
 IC [7]  
 ICM C12P021-06  
 ICS C12P013-04; C07H021-04; C12N001-20; C12N015-74; C12N009-10  
 IPCI C12P0021-06 [ICM,7]; C12P0013-04 [ICS,7]; C12P0013-00 [ICS,7,C\*];  
 C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C\*]; C12N0001-20 [ICS,7];  
 C12N0015-74 [ICS,7]; C12N0009-10 [ICS,7]  
 IPCR C07H0021-00 [I,C\*]; C07H0021-04 [I,A]; C07K0014-195 [I,C\*];  
 C07K0014-34 [I,A]; C12N0001-20 [I,C\*]; C12N0001-20 [I,A];  
 C12N0009-00 [I,C\*]; C12N0009-00 [I,A]; C12N0009-10 [I,C\*];  
 C12N0009-10 [I,A]; C12N0015-74 [I,C\*]; C12N0015-74 [I,A];  
 C12P0013-00 [I,C\*]; C12P0013-04 [I,A]; C12P0021-06 [I,C\*];  
 C12P0021-06 [I,A]  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.  
 L5 ANSWER 13 OF 27 USPATFULL on STN  
 AN 2005:268092 USPATFULL  
 TI Modified bacterial surface layer proteins  
 IN Pouwels, Pieter Hendrik, Rijswijk, NETHERLANDS  
 Smit, Egbert, Sittard, NETHERLANDS  
 Tielen, Frans, Prinsenbeek, NETHERLANDS  
 PI US 20050233408 A1 20051020  
 AI US 2003-500307 A1 20021223 (10)  
 WO 2002-EP14749 20021223  
 20041122 PCT 371 date  
 PRAI EP 2001-310937 20011228  
 DT Utility  
 FS APPLICATION  
 LN.CNT 2664  
 INCL INCLM: 435/034.000  
 INCLS: 530/395.000; 435/252.300  
 NCL NCLM: 435/034.000  
 NCLS: 435/252.300; 530/395.000  
 IC [7]  
 ICM C12Q001-04  
 ICS C12N001-21; C07K014-335  
 IPCI C12Q0001-04 [ICM,7]; C12N0001-21 [ICS,7]; C07K0014-335 [ICS,7];  
 C07K0014-195 [ICS,7,C\*]

IPCR C12N0015-09 [I,C\*]; C12N0015-09 [I,A]; A61K0039-02 [I,C\*];  
A61K0039-02 [I,A]; A61P0031-00 [I,C\*]; A61P0031-04 [I,A];  
C07K0014-195 [I,C\*]; C07K0014-335 [I,A]; C12N0001-15 [I,C\*];  
C12N0001-15 [I,A]; C12N0001-19 [I,C\*]; C12N0001-19 [I,A];  
C12N0001-20 [I,C\*]; C12N0001-20 [I,A]; C12N0001-21 [I,C\*];  
C12N0001-21 [I,A]; C12N0005-10 [I,C\*]; C12N0005-10 [I,A];  
C12N0015-31 [I,C\*]; C12N0015-31 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 14 OF 27 USPATFULL on STN

AN 2005:220997 USPATFULL

TI Corynebacterium glutamicum genes encoding proteins involved in  
homeostasis and adaptation

IN Pompejus, Markus, Waldsee, GERMANY, FEDERAL REPUBLIC OF  
Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF  
Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF  
Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF

PA Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF  
BASF Aktiengesellschaft, Ludwigshafen, GERMANY, FEDERAL REPUBLIC OF,  
D-67056 (non-U.S. corporation)

PI US 20050191732 A1 20050901

AI US 2003-721922 A1 20031124 (10)

RLI Continuation of Ser. No. US 2000-603124, filed on 23 Jun 2000, ABANDONED

PRAI DE 1999-19931418 19990708  
DE 1999-19932124 19990709  
DE 1999-19932126 19990709  
DE 1999-19932127 19990709  
DE 1999-19932133 19990709  
DE 1999-19932207 19990709  
DE 1999-19932208 19990709  
DE 1999-19932225 19990709  
DE 1999-19932229 19990709  
DE 1999-19932914 19990709  
DE 1999-19933006 19990709  
DE 1999-19940765 19990827  
DE 1999-19940768 19990827  
DE 1999-19940831 19990827  
DE 1999-19940832 19990827  
DE 1999-19941385 19990831  
DE 1999-19941396 19990831  
DE 1999-19942087 19990903  
US 1999-141031P 19990625 (60)  
US 1999-143694P 19990714 (60)  
US 1999-151778P 19990831 (60)

DT Utility

FS APPLICATION

LN.CNT 6552

INCL INCLM: 435/106.000  
INCLS: 435/006.000; 435/069.100; 435/193.000; 435/252.300; 435/320.100;  
536/023.200

NCL NCLM: 435/106.000  
NCLS: 435/006.000; 435/069.100; 435/193.000; 435/252.300; 435/320.100;  
536/023.200

IC [7]

ICM C12Q001-68  
ICS C07H021-04; C12P013-04; C12N009-10; C12N001-21; C12N015-74  
IPCI C12Q001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C\*];  
C12P0013-04 [ICS,7]; C12P0013-00 [ICS,7,C\*]; C12N0009-10 [ICS,7];  
C12N0001-21 [ICS,7]; C12N0015-74 [ICS,7]  
IPCR C07H0021-00 [I,C\*]; C07H0021-04 [I,A]; C07K0014-195 [I,C\*];  
C07K0014-34 [I,A]; C12N0001-21 [I,C\*]; C12N0001-21 [I,A];  
C12N0009-00 [I,C\*]; C12N0009-00 [I,A]; C12N0009-10 [I,C\*];

C12N0009-10 [I,A]; C12N0015-74 [I,C\*]; C12N0015-74 [I,A];  
C12P0001-04 [I,C\*]; C12P0001-04 [I,A]; C12P0013-00 [I,C\*];  
C12P0013-04 [I,A]; C12Q0001-68 [I,C\*]; C12Q0001-68 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 15 OF 27 USPATFULL on STN  
AN 2005:158196 USPATFULL  
TI Nucleic acid and amino acid sequences relating to streptococcus  
pneumoniae for diagnostics and therapeutics  
IN Doucette-Stamm, Lynn A., Framingham, MA, UNITED STATES  
Bush, David, Somerville, MA, UNITED STATES  
PI US 20050136404 A1 20050623  
AI US 2003-617320 A1 20030710 (10)  
RLI Division of Ser. No. US 1998-107433, filed on 30 Jun 1998, PENDING  
PRAI US 1997-51553P 19970702 (60)  
US 1998-85131P 19980512 (60)  
DT Utility  
FS APPLICATION  
LN.CNT 12957  
INCL INCLM: 435/006.000  
INCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.700  
NCL NCLM: 435/006.000  
NCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.700  
IC [7]  
ICM C12Q001-68  
ICS C07H021-04; C12N001-21; C07K014-315  
IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C\*];  
C12N0001-21 [ICS,7]; C07K0014-315 [ICS,7]; C07K0014-195  
[ICS,7,C\*]  
IPCR C07H0021-00 [I,C\*]; C07H0021-02 [I,A]; C07H0021-04 [I,A];  
C07K0014-195 [I,C\*]; C07K0014-315 [I,A]  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 16-20

L5 ANSWER 16 OF 27 USPATFULL on STN  
AN 2005:131152 USPATFULL  
TI Lactobacillus acidophilus nucleic acid sequences encoding cell surface  
protein homologues and uses therefore  
IN Klaenhammer, Todd R., Raleigh, NC, UNITED STATES  
Alterman, Eric, Apex, NC, UNITED STATES  
Buck, B. Logan, Banner Elk, NC, UNITED STATES  
Russell, W. Michael, Newburg, IN, UNITED STATES  
PI US 20050112612 A1 20050526  
US 7348420 B2 20080325  
AI US 2004-831070 A1 20040423 (10)  
PRAI US 2003-465621P 20030425 (60)  
DT Utility  
FS APPLICATION  
LN.CNT 6100  
INCL INCLM: 435/006.000  
INCLS: 435/069.100; 435/183.000; 435/252.300; 435/320.100; 530/350.000;  
536/023.200  
NCL NCLM: 536/023.100; 435/006.000  
NCLS: 435/069.100; 435/252.300; 435/320.100; 435/183.000; 530/350.000;  
536/023.200  
IC [7]  
ICM C12Q001-68  
ICS C07H021-04; C12P021-06; C12N009-00; C12N001-21; C07K014-335  
IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C\*];  
C12P0021-06 [ICS,7]; C12N0009-00 [ICS,7]; C12N0001-21 [ICS,7];

C07K0014-335 [ICS,7]; C07K0014-195 [ICS,7,C\*]  
 IPCI-2 C07H0021-04 [I,A]; C07H0021-00 [I,C\*]; C12N0001-20 [I,A];  
 C12N0015-00 [I,A]; C12P0001-20 [I,A]  
 IPCR C07H0021-00 [I,C]; C07H0021-04 [I,A]; C07K0014-195 [I,C\*];  
 C07K0014-335 [I,A]; C12N0001-20 [I,C]; C12N0001-20 [I,A];  
 C12N0001-21 [I,C\*]; C12N0001-21 [I,A]; C12N0009-00 [I,C\*];  
 C12N0009-00 [I,A]; C12N0015-00 [I,C]; C12N0015-00 [I,A];  
 C12P0021-06 [I,C\*]; C12P0021-06 [I,A]; C12Q0001-68 [I,C\*];  
 C12Q0001-68 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 17 OF 27 USPATFULL on STN  
 AN 2004:95339 USPATFULL  
 TI Nutritional formulations containing synbiotic substances  
 IN Kaup, Susan M., Collingswood, NJ, UNITED STATES  
 Wilson, Jeffrey L., Doylestown, PA, UNITED STATES  
 Kostek, Beverley M., Glen Mills, PA, UNITED STATES  
 Frantz, David C., Pottstown, PA, UNITED STATES  
 PA Wyeth, Madison, NJ, UNITED STATES, 07940 (U.S. corporation)  
 PI US 20040072794 A1 20040415  
 AI US 2003-681658 A1 20031008 (10)  
 PRAI US 2002-418109P 20021011 (60)  
 DT Utility  
 FS APPLICATION  
 LN.CNT 542  
 INCL INCLM: 514/054.000  
 INCLS: 424/093.450  
 NCL NCLM: 514/054.000  
 NCLS: 424/093.450  
 IC [7]  
 ICM A61K045-00  
 ICS A61K031-715  
 IPCI A61K0045-00 [ICM,7]; A61K0031-715 [ICS,7]  
 IPCR A23L0001-052 [I,C\*]; A23L0001-0528 [I,A]; A23L0001-29 [I,C\*];  
 A23L0001-29 [I,A]; A23L0001-30 [I,C\*]; A23L0001-30 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 18 OF 27 USPATFULL on STN  
 AN 2004:12970 USPATFULL  
 TI Polynucleotides, materials incorporating them, and methods for using  
 them  
 IN Glenn, Matthew, Whenuapai, NEW ZEALAND  
 Havukkala, Ilkka J., Remuera, NEW ZEALAND  
 Lubbers, Mark, Palmerston North, NEW ZEALAND  
 Dekker, James, Palmerston North, NEW ZEALAND  
 PA GENESIS RESEARCH AND DEVELOPMENT CORP. LTD., Parnell, NEW ZEALAND  
 (non-U.S. corporation)  
 PI US 20040009490 A1 20040115  
 US 7125698 B2 20061024  
 AI US 2002-264213 A1 20021003 (10)  
 RLI Continuation-in-part of Ser. No. US 2001-971536, filed on 2 Oct 2001,  
 PENDING Continuation-in-part of Ser. No. US 2000-634238, filed on 8 Aug  
 2000, GRANTED, Pat. No. US 6544772  
 PRAI US 1999-147853P 19990809 (60)  
 US 1999-147852P 19990809 (60)  
 US 1999-152032P 19990901 (60)  
 US 1999-152031P 19990901 (60)  
 DT Utility  
 FS APPLICATION  
 LN.CNT 5375  
 INCL INCLM: 435/006.000  
 INCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.200



NCL NCLM: 435/193.000; 435/006.000  
 NCLS: 426/534.000; 435/183.000; 435/194.000; 530/350.000; 435/069.100;  
 435/252.300; 435/320.100; 536/023.200

IC [7]  
 ICM C12Q001-68  
 ICS C07H021-04; C12P021-02; C12N001-21; C12N015-74; C07K014-335  
 IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C\*];  
 C12P0021-02 [ICS,7]; C12N0001-21 [ICS,7]; C12N0015-74 [ICS,7];  
 C07K0014-335 [ICS,7]; C07K0014-195 [ICS,7,C\*]  
 IPCI-2 C12N0009-10 [I,A]  
 IPCR C12N0009-10 [I,C]; C12N0009-10 [I,A]; A23C0019-00 [I,C\*];  
 A23C0019-032 [I,A]; A61K0038-00 [N,C\*]; A61K0038-00 [N,A];  
 C07K0014-195 [I,C\*]; C07K0014-335 [I,A]; C12N0001-21 [I,C\*];  
 C12N0001-21 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 19 OF 27 USPATFULL on STN  
 AN 2004:250212 USPATFULL  
 TI Nucleic acid and amino acid sequences relating to Streptococcus  
 pneumoniae for diagnostics and therapeutics  
 IN Doucette-Stamm, Lynn A., Framingham, MA, United States  
 Bush, David, Somerville, MA, United States  
 PA Genome Therapeutics Corporation, Waltham, MA, United States (U.S.  
 corporation)  
 PI US 6800744 B1 20041005  
 AI US 1998-107433 19980630 (9)  
 PRAI US 1998-85131P 19980512 (60)  
 US 1997-51553P 19970702 (60)  
 DT Utility  
 FS GRANTED  
 LN.CNT 11545  
 INCL INCLM: 536/023.100  
 INCLS: 435/006.000; 435/320.100; 435/325.000; 435/254.000; 435/419.000;  
 536/024.100; 536/023.400; 536/024.320

NCL NCLM: 536/023.100  
 NCLS: 435/006.000; 435/320.100; 435/325.000; 435/419.000; 536/023.400;  
 536/024.100; 536/024.320

IC [7]  
 ICM C12Q001-68  
 ICS C12N001-14; C12N015-00; C12N005-00; C12N005-04; C07H021-02;  
 C07H021-04  
 IPCI C12Q0001-68 [ICM,7]; C12N0001-14 [ICS,7]; C12N0015-00 [ICS,7];  
 C12N0005-00 [ICS,7]; C12N0005-04 [ICS,7]; C07H0021-02 [ICS,7];  
 C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C\*]  
 IPCR C07H0021-00 [I,C\*]; C07H0021-02 [I,A]; C07H0021-04 [I,A];  
 C07K0014-195 [I,C\*]; C07K0014-315 [I,A]

EXF 536/23.1; 536/23.4; 536/24.32; 435/320.1; 435/325; 435/254.11; 435/419;  
 435/6

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 20 OF 27 USPATFULL on STN  
 AN 2003:71519 USPATFULL  
 TI Corynebacterium glutamicum genes encoding metabolic pathway proteins  
 IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF  
 Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF  
 Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF  
 Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF  
 Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF  
 Kim, Jun-Won, Seoul, KOREA, REPUBLIC OF  
 Lee, Heung-Shick, Seoul, KOREA, REPUBLIC OF  
 Hwang, Byung-Joon, Seoul, KOREA, REPUBLIC OF

PI US 20030049804 A1 20030313

AI US 2000-746660 A1 20001222 (9)  
 RLI Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,  
 PENDING Continuation-in-part of Ser. No. US 2000-603124, filed on 23 Jun  
 2000, PENDING  
 PRAI DE 1999-19931420 19990708  
 US 1999-141031P 19990625 (60)  
 US 1999-142101P 19990702 (60)  
 US 1999-148613P 19990812 (60)  
 US 2000-187970P 20000309 (60)  
 DT Utility  
 FS APPLICATION  
 LN.CNT 15004  
 INCL INCLM: 435/115.000  
 INCLS: 435/069.100; 435/252.300; 435/320.100; 435/183.000; 536/023.200  
 NCL NCLM: 435/115.000  
 NCLS: 435/069.100; 435/183.000; 435/252.300; 435/320.100; 536/023.200  
 IC [7]  
 ICM C12P013-08  
 ICS C07H021-04; C12N009-00; C12P021-02; C12N001-21  
 IPCI C12P0013-08 [ICM,7]; C12P0013-00 [ICM,7,C\*]; C07H0021-04 [ICS,7];  
 C07H0021-00 [ICS,7,C\*]; C12N0009-00 [ICS,7]; C12P0021-02 [ICS,7];  
 C12N0001-21 [ICS,7]  
 IPCR C07K0014-195 [I,C\*]; C07K0014-34 [I,A]; C12N0001-21 [I,C\*];  
 C12N0001-21 [I,A]; C12N0009-00 [I,C\*]; C12N0009-00 [I,A];  
 C12N0009-18 [I,C\*]; C12N0009-18 [I,A]; C12N0009-90 [I,C\*];  
 C12N0009-90 [I,A]  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 17

L5 ANSWER 17 OF 27 USPATFULL on STN  
 AN 2004:95339 USPATFULL  
 TI Nutritional formulations containing synbiotic substances  
 IN Kaup, Susan M., Collingswood, NJ, UNITED STATES  
 Wilson, Jeffrey L., Doylestown, PA, UNITED STATES  
 Kostek, Beverley M., Glen Mills, PA, UNITED STATES  
 Frantz, David C., Pottstown, PA, UNITED STATES  
 PA Wyeth, Madison, NJ, UNITED STATES, 07940 (U.S. corporation)  
 PI US 20040072794 A1 20040415  
 AI US 2003-681658 A1 20031008 (10)  
 PRAI US 2002-418109P 20021011 (60)  
 DT Utility  
 FS APPLICATION  
 LN.CNT 542  
 INCL INCLM: 514/054.000  
 INCLS: 424/093.450  
 NCL NCLM: 514/054.000  
 NCLS: 424/093.450  
 IC [7]  
 ICM A61K045-00  
 ICS A61K031-715  
 IPCI A61K0045-00 [ICM,7]; A61K0031-715 [ICS,7]  
 IPCR A23L0001-052 [I,C\*]; A23L0001-0528 [I,A]; A23L0001-29 [I,C\*];  
 A23L0001-29 [I,A]; A23L0001-30 [I,C\*]; A23L0001-30 [I,A]  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 17 ab

L5 ANSWER 17 OF 27 USPATFULL on STN  
 AB Nutritional compositions are provided which comprise oligofructose,

sialyllactose and probiotic bacteria, which are useful in the eradication of pathogenic microorganisms in the gastrointestinal tracts of patients.

=> d 15 17 kwic

L5 ANSWER 17 OF 27 USPATFULL on STN

SUMM [0004] Prebiotics are nondigestible food ingredients that that beneficially affect the host by selectively stimulating the growth and/or activity of one or a limited number. . . .

SUMM [0011] Sialyllactose is known to have anti-adhesive properties for specific pathogenic bacteria. For example, sialyllactose acts to inhibit cholera toxin invitro (Idota et al., "Inhibition of Cholera Toxin by Human Milk Fractions and Sialyllactose," Biosci. Biotech. Biochem. 59:417-419) and Helicobacter pylori (Simon et al., "Inhibition of Helicobacter pylori Binding to Gastrointestinal Epithelial Cells by Sialic Acid-Containing Oligosaccharides," Infection and Immunity, 750-757, (1997)).

SUMM [0015] Probiotics are live microbial food ingredients that have a beneficial effect on human health. (Salminen et al., "Functional food science and gastrointestinal physiology and function." Brit. J. Nutr. 80(suppl. 1):S147-S171 (1998)).

SUMM . . . . carbohydrate to lactic acid. The specific strains most often studied include members of the genera Lactobacillus and Bifidobacterium. (Sanders, "Probiotics." Food Technol. 53:67-77 (1999)).

SUMM [0017] Some lactic acid bacteria specifically produce lactic acid as a major product of their metabolism. Some produce predominantly the levorotary "L"-form of lactic acid [L(+)-lactic acid], others produce predominantly the dextrorotary "D"-form. . . .

SUMM [0019] A milk product containing LGG significantly shortened the duration of diarrhea in young children. (Kaila et al., "Enhancement of the circulating antibody secreting. . . .

SUMM [0021] U.S. Pat. No. 5,908,646 discloses a method for inhibiting the growth or activity of Clostridium species in a human food product by adding an effective amount of the beneficial microorganism, L. rhamnosus [L. casei subspecies rhamnosus], which produces predominantly L(+)-lactic acid.

SUMM . . . . viable cells of three specific microorganisms beneficial to the human intestinal microorganisms for preventing diarrhea. Specifically, the three microorganisms are Lactobacillus reuteri, Lactobacillus acidophilus and Bifidobacterium infantis. The diarrhea can be caused by antibiotic treatment or by infection with a virus, a. . . .

SUMM . . . . "Bifidobacterium bifidum." (Fukushima et al., "Effect of a probiotic formula on intestinal immunoglobulin A production in healthy children." Int. J. Food Microb. 42-39-44 (1998)).

=> d 15 18

L5 ANSWER 18 OF 27 USPATFULL on STN

AN 2004:12970 USPATFULL

TI Polynucleotides, materials incorporating them, and methods for using them

IN Glenn, Matthew, Whenuapai, NEW ZEALAND  
Havukkala, Ilkka J., Remuera, NEW ZEALAND  
Lubbers, Mark, Palmerston North, NEW ZEALAND  
Dekker, James, Palmerston North, NEW ZEALAND

PA GENESIS RESEARCH AND DEVELOPMENT CORP. LTD., Parnell, NEW ZEALAND (non-U.S. corporation)

PI US 20040009490 A1 20040115  
US 7125698 B2 20061024

AI US 2002-264213 A1 20021003 (10)  
 RLI Continuation-in-part of Ser. No. US 2001-971536, filed on 2 Oct 2001,  
 PENDING Continuation-in-part of Ser. No. US 2000-634238, filed on 8 Aug  
 2000, GRANTED, Pat. No. US 6544772  
 PRAI US 1999-147853P 19990809 (60)  
 US 1999-147852P 19990809 (60)  
 US 1999-152032P 19990901 (60)  
 US 1999-152031P 19990901 (60)  
 DT Utility  
 FS APPLICATION  
 LN.CNT 5375  
 INCL INCLM: 435/006.000  
 INCLS: 435/069.100; 435/252.300; 435/320.100; 530/350.000; 536/023.200  
 NCL NCLM: 435/193.000; 435/006.000  
 NCLS: 426/534.000; 435/183.000; 435/194.000; 530/350.000; 435/069.100;  
 435/252.300; 435/320.100; 536/023.200  
 IC [7]  
 ICM C12Q001-68  
 ICS C07H021-04; C12P021-02; C12N001-21; C12N015-74; C07K014-335  
 IPCI C12Q0001-68 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C\*];  
 C12P0021-02 [ICS,7]; C12N0001-21 [ICS,7]; C12N0015-74 [ICS,7];  
 C07K0014-335 [ICS,7]; C07K0014-195 [ICS,7,C\*]  
 IPCI-2 C12N0009-10 [I,A]  
 IPCR C12N0009-10 [I,C]; C12N0009-10 [I,A]; A23C0019-00 [I,C\*];  
 A23C0019-032 [I,A]; A61K0038-00 [N,C\*]; A61K0038-00 [N,A];  
 C07K0014-195 [I,C\*]; C07K0014-335 [I,A]; C12N0001-21 [I,C\*];  
 C12N0001-21 [I,A]  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 19

L5 ANSWER 19 OF 27 USPATFULL on STN  
 AN 2004:250212 USPATFULL  
 TI Nucleic acid and amino acid sequences relating to Streptococcus  
 pneumoniae for diagnostics and therapeutics  
 IN Doucette-Stamm, Lynn A., Framingham, MA, United States  
 Bush, David, Somerville, MA, United States  
 PA Genome Therapeutics Corporation, Waltham, MA, United States (U.S.  
 corporation)  
 PI US 6800744 B1 20041005  
 AI US 1998-107433 19980630 (9)  
 PRAI US 1998-85131P 19980512 (60)  
 US 1997-51553P 19970702 (60)  
 DT Utility  
 FS GRANTED  
 LN.CNT 11545  
 INCL INCLM: 536/023.100  
 INCLS: 435/006.000; 435/320.100; 435/325.000; 435/254.000; 435/419.000;  
 536/024.100; 536/023.400; 536/024.320  
 NCL NCLM: 536/023.100  
 NCLS: 435/006.000; 435/320.100; 435/325.000; 435/419.000; 536/023.400;  
 536/024.100; 536/024.320  
 IC [7]  
 ICM C12Q001-68  
 ICS C12N001-14; C12N015-00; C12N005-00; C12N005-04; C07H021-02;  
 C07H021-04  
 IPCI C12Q0001-68 [ICM,7]; C12N0001-14 [ICS,7]; C12N0015-00 [ICS,7];  
 C12N0005-00 [ICS,7]; C12N0005-04 [ICS,7]; C07H0021-02 [ICS,7];  
 C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C\*]  
 IPCR C07H0021-00 [I,C\*]; C07H0021-02 [I,A]; C07H0021-04 [I,A];  
 C07K0014-195 [I,C\*]; C07K0014-315 [I,A]

EXF 536/23.1; 536/23.4; 536/24.32; 435/320.1; 435/325; 435/254.11; 435/419;  
435/6

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 20-28

L5 ANSWER 20 OF 27 USPATFULL on STN

AN 2003:71519 USPATFULL

TI Corynebacterium glutamicum genes encoding metabolic pathway proteins

IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF

Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF

Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF

Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF

Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF

Kim, Jun-Won, Seoul, KOREA, REPUBLIC OF

Lee, Heung-Shick, Seoul, KOREA, REPUBLIC OF

Hwang, Byung-Joon, Seoul, KOREA, REPUBLIC OF

PI US 20030049804 A1 20030313

AI US 2000-746660 A1 20001222 (9)

RLI Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,  
PENDING Continuation-in-part of Ser. No. US 2000-603124, filed on 23 Jun  
2000, PENDING

PRAI DE 1999-19931420 19990708

US 1999-141031P 19990625 (60)

US 1999-142101P 19990702 (60)

US 1999-148613P 19990812 (60)

US 2000-187970P 20000309 (60)

DT Utility

FS APPLICATION

LN.CNT 15004

INCL INCLM: 435/115.000

INCLS: 435/069.100; 435/252.300; 435/320.100; 435/183.000; 536/023.200

NCL NCLM: 435/115.000

NCLS: 435/069.100; 435/183.000; 435/252.300; 435/320.100; 536/023.200

IC [7]

ICM C12P013-08

ICS C07H021-04; C12N009-00; C12P021-02; C12N001-21

IPCI C12P0013-08 [ICM,7]; C12P0013-00 [ICM,7,C\*]; C07H0021-04 [ICS,7];  
C07H0021-00 [ICS,7,C\*]; C12N0009-00 [ICS,7]; C12P0021-02 [ICS,7];  
C12N0001-21 [ICS,7]

IPCR C07K0014-195 [I,C\*]; C07K0014-34 [I,A]; C12N0001-21 [I,C\*];  
C12N0001-21 [I,A]; C12N0009-00 [I,C\*]; C12N0009-00 [I,A];  
C12N0009-18 [I,C\*]; C12N0009-18 [I,A]; C12N0009-90 [I,C\*];  
C12N0009-90 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 21 OF 27 USPATFULL on STN

AN 2003:95966 USPATFULL

TI Polynucleotides, materials incorporating them, and methods for using  
them

IN Glenn, Matthew, Auckland, NEW ZEALAND

Havukkala, Ilkka J., Auckland, NEW ZEALAND

Bloksberg, Leonard N., Auckland, NEW ZEALAND

Lubbers, Mark W., Palmerston North, NEW ZEALAND

Dekker, James, Palmerston North, NEW ZEALAND

Christensson, Anna C., Lund, SWEDEN

Holland, Ross, Palmerson North, NEW ZEALAND

O'Toole, Paul W., Palmerston North, NEW ZEALAND

Reid, Julian R., Palmerston North, NEW ZEALAND

Coolbear, Timothy, Palmerston North, NEW ZEALAND

PA Genesis Research & Development Corp. Ltd, Parnell, NEW ZEALAND (non-U.S.)

corporation)  
 Via Lachia Bioscience (NZ) Ltd., Auckland, NEW ZEALAND (non-U.S.  
 corporation)  
 PI US 6544772 B1 20030408  
 AI US 2000-634238 20000808 (9)  
 DT Utility  
 FS GRANTED  
 LN.CNT 2015  
 INCL INCLM: 435/252.300  
 INCLS: 435/320.100; 536/023.700  
 NCL NCLM: 435/252.300  
 NCLS: 435/320.100; 536/023.700  
 IC [7]  
 ICM C12N001-21  
 ICS C12N015-63; C12N015-31  
 IPCI C12N0001-21 [ICM,7]; C12N0015-63 [ICS,7]; C12N0015-31 [ICS,7]  
 IPCR A23C0019-00 [I,C\*]; A23C0019-032 [I,A]; C07K0014-195 [I,C\*];  
 C07K0014-335 [I,A]; C12N0001-21 [I,C\*]; C12N0001-21 [I,A];  
 C12N0015-31 [I,C\*]; C12N0015-31 [I,A]  
 EXF 435/252.3; 435/320.1; 536/23.7  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 22 OF 27 BIOTECHDS COPYRIGHT 2008 THOMSON REUTERS on STN  
 AN 1999-00562 BIOTECHDS  
 TI Use of lactic and propionic acid bacteria;  
 to bind mycotoxin to prevent their absorption or to purify  
 contaminated food or feedstuff  
 AU El-Nezami H; Kankaanpaa P; Salminen S; Ahokas J  
 PA Roy.Melbourne-Inst.Technol.  
 LO Melbourne, Victoria, Australia.  
 PI WO 9834503 13 Aug 1998  
 AI WO 1998-AU63 6 Feb 1998  
 PRAI AU 1997-5005 7 Feb 1997  
 DT Patent  
 LA English  
 OS WPI: 1998-557001 [49]

L5 ANSWER 23 OF 27 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): CP000705 GenBank (R)  
 GenBank ACC. NO. (GBN): CP000705 AAOV01000000 AAOV01000001-AAOV01000097  
 GenBank VERSION (VER): CP000705.1 GI:148530277  
 SEQUENCE LENGTH (SQL): 1999618  
 MOLECULE TYPE (CI): DNA; circular  
 DIVISION CODE (CI): Bacteria  
 DATE (DATE): 17 Oct 2007  
 DEFINITION (DEF): Lactobacillus reuteri F275,  
 complete genome.  
 SOURCE: Lactobacillus reuteri F275  
 ORGANISM (ORGN): Lactobacillus reuteri F275  
 Bacteria; Firmicutes; Lactobacillales;  
 Lactobacillaceae; Lactobacillus  
 PROJECT (PJID): GenomeProject:15766  
 COMMENT:  
 URL -- <http://www.jgi.doe.gov>  
 JGI Project ID: 4000135  
 Source DNA available from Gerald Tannock  
 (gerald.tannock@stonebow.otago.ac.nz)  
 Bacteria available from DSMZ: DSM 20016  
 Contacts: Gerald Tannock (gerald.tannock@stonebow.otago.ac.nz)  
 Paul Richardson (microbes@cuba.jgi-psf.org)  
 Quality assurance done by JGI-Stanford

Annotation done by JGI-ORNL and JGI-PGF

Finishing done by JGI-PGF

Finished microbial genomes have been curated to close all gaps with greater than 98% coverage of at least two independent clones. Each base pair has a minimum q (quality) value of 30 and the total error rate is less than one per 50000.

The JGI and collaborators endorse the principles for the distribution and use of large scale sequencing data adopted by the larger genome sequencing community and urge users of this data to follow them. It is our intention to publish the work of this project in a timely fashion and we welcome collaborative interaction on the project and analysis.

(<http://www.genome.gov/page.cfm?pageID=10506376>).

REFERENCE: 1 (bases 1 to 1999618)  
AUTHOR (AU): Copeland,A.; Lucas,S.; Lapidus,A.; Barry,K.;  
Detter,J.C.; Glavina del Rio,T.; Hammon,N.; Israni,S.;  
Dalin,E.; Tice,H.; Pitluck,S.; Goltsman,E.; Schmutz,J.;  
Larimer,F.; Land,M.; Hauser,L.; Kyrpides,N.; Kim,E.;  
Walter,J.; Heng,N.C.K.; Tannock,G.W.; Richardson,P.  
TITLE (TI): Complete sequence of chromosome of  
Lactobacillus reuteri DSM 20016  
JOURNAL (SO): Unpublished  
REFERENCE: 2 (bases 1 to 1999618)  
AUTHOR (AU): Copeland,A.; Lucas,S.; Lapidus,A.; Barry,K.;  
Detter,J.C.; Glavina del Rio,T.; Hammon,N.; Israni,S.;  
Dalin,E.; Tice,H.; Pitluck,S.; Goltsman,E.; Schmutz,J.;  
Larimer,F.; Land,M.; Hauser,L.; Kyrpides,N.; Kim,E.;  
Walter,J.; Heng,N.C.K.; Tannock,G.W.; Richardson,P.  
TITLE (TI): Direct Submission  
JOURNAL (SO): Submitted (17-MAY-2007) US DOE Joint Genome Institute,  
2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698,  
USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1999618	/organism="Lactobacillus reuteri F275" /mol-type="genomic DNA" /strain="DSM 20016" /db-xref="taxon:299033" /note="F275 = DSM 20016 = JCM 1112"

L5 ANSWER 24 OF 27 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): AM270397 GenBank (R)  
GenBank ACC. NO. (GBN): AM270397  
GenBank VERSION (VER): AM270397.1 GI:134084136  
CAS REGISTRY NO. (RN): 928607-03-8  
SEQUENCE LENGTH (SQL): 163680  
MOLECULE TYPE (CI): DNA; linear  
DIVISION CODE (CI): Plants, fungi, algae  
DATE (DATE): 24 Mar 2007  
DEFINITION (DEF): Aspergillus niger contig An18c0040, complete genome.  
SOURCE: Aspergillus niger  
ORGANISM (ORGN): Aspergillus niger  
Eukaryota; Fungi; Ascomycota; Pezizomycotina;  
Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic  
Trichocomaceae; Aspergillus  
REFERENCE: 1 (bases 150631 to 153085)

AUTHOR (AU): Habison,A.; Kubicek,C.P.; Rohr,M.  
 TITLE (TI): Partial purification and regulatory properties of  
 phosphofructokinase from *Aspergillus niger*  
 JOURNAL (SO): Biochem. J., 209 (3), 669-676 (1983)  
 OTHER SOURCE (OS): CA 99:171737  
 REFERENCE: 2 (bases 71863 to 73356)  
 AUTHOR (AU): Manney,T.R.  
 TITLE (TI): Expression of the BAR1 gene in *Saccharomyces*  
*cerevisiae*: induction by the alpha mating pheromone of  
 an activity associated with a secreted protein  
 JOURNAL (SO): J. Bacteriol., 155 (1), 291-301 (1983)  
 OTHER SOURCE (OS): CA 99:102121  
 REFERENCE: 3 (bases 71863 to 73356)  
 AUTHOR (AU): Jones,E.W.  
 TITLE (TI): The synthesis and function of proteases in  
*Saccharomyces*: genetic approaches  
 JOURNAL (SO): Annu. Rev. Genet., 18, 233-270 (1984)  
 OTHER SOURCE (OS): CA 102:92538  
 REFERENCE: 4 (bases 144032 to 145578)  
 AUTHOR (AU): Brandsch,R.; Bichler,V.  
 TITLE (TI): In vivo and in vitro expression of the  
 6-hydroxy-D-nicotine oxidase gene of *Arthrobacter*  
*oxidans*, cloned into *Escherichia coli*, as an  
 enzymatically active, covalently flavinylated  
 polypeptide  
 JOURNAL (SO): FEBS Lett., 192 (2), 204-208 (1985)  
 OTHER SOURCE (OS): CA 104:29597  
 REFERENCE: 5 (bases 150631 to 153085)  
 AUTHOR (AU): Schreferl,G.; Kubicek,C.P.; Rohr,M.  
 TITLE (TI): Inhibition of citric acid accumulation by manganese  
 ions in *Aspergillus niger* mutants with reduced citrate  
 control of phosphofructokinase  
 JOURNAL (SO): J. Bacteriol., 165 (3), 1019-1022 (1986)  
 OTHER SOURCE (OS): CA 104:165023  
 REFERENCE: 6 (bases 156827 to 158638)  
 AUTHOR (AU): Whittington,H.A.; Grant,S.; Roberts,C.F.; Lamb,H.;  
 Hawkins,A.R.  
 TITLE (TI): Identification and isolation of a putative permease  
 gene in the quinic acid utilization (QUT) gene cluster  
 of *Aspergillus nidulans*  
 JOURNAL (SO): Curr. Genet., 12 (2), 135-139 (1987)  
 OTHER SOURCE (OS): CA 107:91128  
 REFERENCE: 7 (bases 54105 to 55762)  
 AUTHOR (AU): Chisholm,V.T.; Lea,H.Z.; Rai,R.; Cooper,T.G.  
 TITLE (TI): Regulation of allantoate transport in wild-type and  
 mutant strains of *Saccharomyces cerevisiae*  
 JOURNAL (SO): J. Bacteriol., 169 (4), 1684-1690 (1987)  
 OTHER SOURCE (OS): CA 106:172689  
 REFERENCE: 8 (bases 71863 to 73356)  
 AUTHOR (AU): MacKay,V.L.; Welch,S.K.; Insley,M.Y.; Manney,T.R.;  
 Holly,J.; Saari,G.C.; Parker,M.L.  
 TITLE (TI): The *Saccharomyces cerevisiae* BAR1 gene encodes an  
 exported protein with homology to pepsin  
 JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 85 (1), 55-59 (1988)  
 OTHER SOURCE (OS): CA 108:125658  
 REFERENCE: 9 (bases 54105 to 55762)  
 AUTHOR (AU): Rai,R.; Genbauffe,F.S.; Cooper,T.G.  
 TITLE (TI): Structure and transcription of the allantoate permease  
 gene (DAL5) from *Saccharomyces cerevisiae*  
 JOURNAL (SO): J. Bacteriol., 170 (1), 266-271 (1988)  
 OTHER SOURCE (OS): CA 109:17930  
 REFERENCE: 10



AUTHOR (AU): Hawkins,A.R.; Lamb,H.K.; Smith,M.; Keyte,J.W.;  
 Roberts,C.F.  
 TITLE (TI): Molecular organisation of the quinic acid utilization  
 (QUT) gene cluster in *Aspergillus nidulans*  
 JOURNAL (SO): Mol. Gen. Genet., 214 (2), 224-231 (1988)  
 OTHER SOURCE (OS): CA 111:188522  
 REFERENCE: 11 (bases 68231 to 69040)  
 AUTHOR (AU): Honjo,M.; Nakayama,A.; Fukazawa,K.; Kawamura,K.;  
 Ando,K.; Furutani,Y.  
 TITLE (TI): A novel *Bacillus subtilis* gene involved in negative  
 control of sporulation and degradative-enzyme  
 production  
 JOURNAL (SO): J. Bacteriol., 172 (4), 1783-1790 (1990)  
 OTHER SOURCE (OS): CA 113:146166  
 REFERENCE: 12 (bases 5212 to 7379)  
 AUTHOR (AU): Nikawa,J.; Hosaka,K.; Tsukagoshi,Y.; Yamashita,S.  
 TITLE (TI): Primary structure of the yeast choline transport gene  
 and regulation of its expression  
 JOURNAL (SO): J. Biol. Chem., 265 (26), 15996-16003 (1990)  
 OTHER SOURCE (OS): CA 114:18549  
 REFERENCE: 13 (bases 159975 to 161849)  
 AUTHOR (AU): Fling,M.E.; Kopf,J.; Tamarkin,A.; Gorman,J.A.;  
 Smith,H.A.; Koltin,Y.  
 TITLE (TI): Analysis of a *Candida albicans* gene that encodes a  
 novel mechanism for resistance to benomyl and  
 methotrexate  
 JOURNAL (SO): Mol. Gen. Genet., 227 (2), 318-329 (1991)  
 OTHER SOURCE (OS): CA 116:100405  
 REFERENCE: 14 (bases 28874 to 30837)  
 AUTHOR (AU): Masuda,N.; Kitamura,N.; Saito,K.  
 TITLE (TI): Primary structure of protein moiety of *Penicillium*  
*notatum* phospholipase B deduced from the cDNA  
 JOURNAL (SO): Eur. J. Biochem., 202 (3), 783-787 (1991)  
 OTHER SOURCE (OS): CA 118:76020  
 REFERENCE: 15 (bases 100363 to 101496)  
 AUTHOR (AU): Sakoda,H.; Imanaka,T.  
 TITLE (TI): Cloning and sequencing of the gene coding for alcohol  
 dehydrogenase of *Bacillus stearothermophilus* and  
 rational shift of the optimum pH  
 JOURNAL (SO): J. Bacteriol., 174 (4), 1397-1402 (1992)  
 OTHER SOURCE (OS): CA 118:186708  
 REFERENCE: 16 (bases 20773 to 22555)  
 AUTHOR (AU): Kamoda,S.; Saburi,Y.  
 TITLE (TI): Structural and enzymatical comparison of  
 lignostilbene- $\alpha$ , $\beta$ -dioxygenase isozymes, I, II,  
 and III, from *Pseudomonas paucimobilis* TMY1009  
 JOURNAL (SO): Biosci. Biotechnol. Biochem., 57 (6), 931-934 (1993)  
 OTHER SOURCE (OS): CA 119:154577  
 REFERENCE: 17 (bases 80602 to 83154)  
 AUTHOR (AU): ElBerry,H.M.; Majumdar,M.L.; Cunningham,T.S.;  
 Sumrada,R.A.; Cooper,T.G.  
 TITLE (TI): Regulation of the urea active transporter gene (DUR3)  
 in *Saccharomyces cerevisiae*  
 JOURNAL (SO): J. Bacteriol., 175 (15), 4688-4698 (1993)  
 OTHER SOURCE (OS): CA 119:242524  
 REFERENCE: 18 (bases 23096 to 24052)  
 AUTHOR (AU): Roper,D.I.; Cooper,R.A.  
 TITLE (TI): Purification, nucleotide sequence and some properties  
 of a bifunctional isomerase/decarboxylase from the  
 homoprotocatechuate degradative pathway of *Escherichia*  
*coli* C  
 JOURNAL (SO): Eur. J. Biochem., 217 (2), 575-580 (1993)

OTHER SOURCE (OS): CA 119:265270  
REFERENCE: 19 (bases 5212 to 7379)  
AUTHOR (AU): Li,Z.; Brendel,M.  
TITLE (TI): Co-regulation with genes of phospholipid biosynthesis  
of the CTR/HNM1-encoded choline/nitrogen mustard  
permease in *Saccharomyces cerevisiae*  
JOURNAL (SO): Mol. Gen. Genet., 241 (5-6), 680-684 (1993)  
OTHER SOURCE (OS): CA 121:28475  
REFERENCE: 20 (bases 159975 to 161849)  
AUTHOR (AU): Ben-Yaacov,R.; Knoller,S.; Caldwell,G.A.; Becker,J.M.;  
Koltin,Y.  
TITLE (TI): *Candida albicans* gene encoding resistance to benomyl  
and methotrexate is a multidrug resistance gene  
JOURNAL (SO): Antimicrob. Agents Chemother., 38 (4), 648-652 (1994)  
OTHER SOURCE (OS): CA 121:2236  
REFERENCE: 21 (bases 150631 to 153085)  
AUTHOR (AU): Legisa,M.; Bencina,M.  
TITLE (TI): Evidence for the activation of 6-phosphofructo-1-kinase  
by cAMP-dependent protein kinase in *Aspergillus niger*  
JOURNAL (SO): FEMS Microbiol. Lett., 118 (3), 327-333 (1994)  
OTHER SOURCE (OS): CA 121:102759  
REFERENCE: 22 (bases 138020 to 140061)  
AUTHOR (AU): Kim,Y.J.; Bjorklund,S.; Li,Y.; Sayre,M.H.;  
Kornberg,R.D.  
TITLE (TI): A multiprotein mediator of transcriptional activation  
and its interaction with the C-terminal repeat domain  
of RNA polymerase II  
JOURNAL (SO): Cell, 77 (4), 599-608 (1994)  
OTHER SOURCE (OS): CA 121:102149  
REFERENCE: 23 (bases 38805 to 39836)  
AUTHOR (AU): Downs,D.M.; Petersen,L.  
TITLE (TI): *apbA*, a new genetic locus involved in thiamine  
biosynthesis in *Salmonella typhimurium*  
JOURNAL (SO): J. Bacteriol., 176 (16), 4858-4864 (1994)  
OTHER SOURCE (OS): CA 121:197350  
REFERENCE: 24 (bases 5212 to 7379)  
AUTHOR (AU): Li,Z.; Brendel,M.  
TITLE (TI): Sensitivity to nitrogen mustard in *Saccharomyces*  
*cerevisiae* is independently determined by regulated  
choline permease and DNA repair  
JOURNAL (SO): Mutat. Res., 315 (2), 139-145 (1994)  
OTHER SOURCE (OS): CA 121:198201  
REFERENCE: 25 (bases 85096 to 90863)  
AUTHOR (AU): Szczypka,M.S.; Wemmie,J.A.; Moye-Rowley,W.S.;  
Thiele,D.J.  
TITLE (TI): A yeast metal resistance protein similar to human  
cystic fibrosis transmembrane conductance regulator  
(CFTR) and multidrug resistance-associated protein  
JOURNAL (SO): J. Biol. Chem., 269 (36), 22853-22857 (1994)  
OTHER SOURCE (OS): CA 122:26140  
REFERENCE: 26 (bases 91484 to 93088)  
AUTHOR (AU): Knight,S.A.; Tamai,K.T.; Kosman,D.J.; Thiele,D.J.  
TITLE (TI): Identification and analysis of a *Saccharomyces*  
*cerevisiae* copper homeostasis gene encoding a  
homeodomain protein  
JOURNAL (SO): Mol. Cell. Biol., 14 (12), 7792-7804 (1994)  
OTHER SOURCE (OS): CA 122:73697  
REFERENCE: 27 (bases 85096 to 90863)  
AUTHOR (AU): Wemmie,J.A.; Szczypka,M.S.; Thiele,D.J.;  
Moye-Rowley,W.S.  
TITLE (TI): Cadmium tolerance mediated by the yeast AP-1 protein  
requires the presence of an ATP-binding cassette

transporter-encoding gene, YCF1

JOURNAL (SO): J. Biol. Chem., 269 (51), 32592-32597 (1994)

OTHER SOURCE (OS): CA 121:294343

REFERENCE: 28 (bases 20773 to 22555)

AUTHOR (AU): Kamoda,S.; Saburi,Y.

TITLE (TI): Cloning of a lignostilbene-alpha,beta-dioxygenase isozyme gene from *Pseudomonas paucimobilis* TMY1009

JOURNAL (SO): Biosci. Biotechnol. Biochem., 59 (10), 1866-1868 (1995)

OTHER SOURCE (OS): CA 124:47043

REFERENCE: 29 (bases 85096 to 90863)

AUTHOR (AU): Li,Z.S.; Szczypka,M.; Lu,Y.P.; Thiele,D.J.; Rea,P.A.

TITLE (TI): The yeast cadmium factor protein (YCF1) is a vacuolar glutathione S-conjugate pump

JOURNAL (SO): J. Biol. Chem., 271 (11), 6509-6517 (1996)

OTHER SOURCE (OS): CA 124:226108

REFERENCE: 30 (bases 33419 to 35477)

AUTHOR (AU): Silva,J.C.; Minto,R.E.; Barry,C.E. III; Holland,K.A.; Townsend,C.A.

TITLE (TI): Isolation and characterization of the versicolorin B synthase gene from *Aspergillus parasiticus*. Expansion of the aflatoxin b1 biosynthetic gene cluster

JOURNAL (SO): J. Biol. Chem., 271 (23), 13600-13608 (1996)

OTHER SOURCE (OS): CA 125:50401

REFERENCE: 31 (bases 15614 to 17392)

AUTHOR (AU): Covert,S.F.; Enkerli,J.; Miao,V.P.; VanEtten,H.D.

TITLE (TI): A gene for maackiain detoxification from a dispensable chromosome of *Nectria haematococca*

JOURNAL (SO): Mol. Gen. Genet., 251 (4), 397-406 (1996)

OTHER SOURCE (OS): CA 125:106677

REFERENCE: 32 (bases 131646 to 132375)

AUTHOR (AU): Mitsuhashi,S.; Miyachi,S.

TITLE (TI): Amino acid sequence homology between N- and C-terminal halves of a carbonic anhydrase in *Porphyridium purpureum*, as deduced from the cloned cDNA

JOURNAL (SO): J. Biol. Chem., 271 (45), 28703-28709 (1996)

OTHER SOURCE (OS): CA 125:321312

REFERENCE: 33 (bases 85096 to 90863)

AUTHOR (AU): Li,Z.S.; Lu,Y.P.; Zhen,R.G.; Szczypka,M.; Thiele,D.J.; Rea,P.A.

TITLE (TI): A new pathway for vacuolar cadmium sequestration in *Saccharomyces cerevisiae*: YCF1-catalyzed transport of bis(glutathionato)cadmium

JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 94 (1), 42-47 (1997)

OTHER SOURCE (OS): CA 126:127966

REFERENCE: 34 (bases 1241 to 3043)

AUTHOR (AU): Saito,Y.; Ishii,Y.; Hayashi,H.; Imao,Y.; Akashi,T.; Yoshikawa,K.; Noguchi,Y.; Soeda,S.; Yoshida,M.; Niwa,M.; Hosoda,J.; Shimomura,K.

TITLE (TI): Cloning of genes coding for L-sorbose and L-sorbose dehydrogenases from *Gluconobacter oxydans* and microbial production of 2-keto-L-gulonate, a precursor of L-ascorbic acid, in a recombinant *G. oxydans* strain

JOURNAL (SO): Appl. Environ. Microbiol., 63 (2), 454-460 (1997)

OTHER SOURCE (OS): CA 126:167180

REFERENCE: 35 (bases 150631 to 153085)

AUTHOR (AU): Ruijter,G.J.; Panneman,H.; Visser,J.

TITLE (TI): Overexpression of phosphofructokinase and pyruvate kinase in citric acid-producing *Aspergillus niger*

JOURNAL (SO): Biochim. Biophys. Acta, 1334 (2-3), 317-326 (1997)

OTHER SOURCE (OS): CA 126:222695

REFERENCE: 36 (bases 49850 to 51919)

AUTHOR (AU): Prieto,R.; Woloshuk,C.P.

TITLE (TI): ord1, an oxidoreductase gene responsible for conversion of O-methylsterigmatocystin to aflatoxin in *Aspergillus flavus*  
 JOURNAL (SO): Appl. Environ. Microbiol., 63 (5), 1661-1666 (1997)  
 OTHER SOURCE (OS): CA 127:13942  
 REFERENCE: 37 (bases 17766 to 20491)  
 AUTHOR (AU): Todd,R.B.; Murphy,R.L.; Martin,H.M.; Sharp,J.A.; Davis,M.A.; Katz,M.E.; Hynes,M.J.  
 TITLE (TI): The acetate regulatory gene facB of *Aspergillus nidulans* encodes a Zn(II)2Cys6 transcriptional activator  
 JOURNAL (SO): Mol. Gen. Genet., 254 (5), 495-504 (1997)  
 OTHER SOURCE (OS): CA 127:105007  
 REFERENCE: 38 (bases 71863 to 73356)  
 AUTHOR (AU): Ballensiefen,W.; Schmitt,H.D.  
 TITLE (TI): Periplasmic Bar1 protease of *Saccharomyces cerevisiae* is active before reaching its extracellular destination  
 JOURNAL (SO): Eur. J. Biochem., 247 (1), 142-147 (1997)  
 OTHER SOURCE (OS): CA 127:187926  
 REFERENCE: 39 (bases 52148 to 53720)  
 AUTHOR (AU): Kuroyanagi,N.; Onogi,H.; Wakabayashi,T.; Hagiwara,M.  
 TITLE (TI): Novel SR-protein-specific kinase, SRPK2, disassembles nuclear speckles  
 JOURNAL (SO): Biochem. Biophys. Res. Commun., 242 (2), 357-364 (1998)  
 OTHER SOURCE (OS): CA 128:241040  
 REFERENCE: 40 (bases 113565 to 114733)  
 AUTHOR (AU): MacDiarmid,C.W.; Gardner,R.C.  
 TITLE (TI): Overexpression of the *Saccharomyces cerevisiae* magnesium transport system confers resistance to aluminum ion  
 JOURNAL (SO): J. Biol. Chem., 273 (3), 1727-1732 (1998)  
 OTHER SOURCE (OS): CA 128:177021  
 REFERENCE: 41 (bases 135940 to 137166)  
 AUTHOR (AU): Wang,H.Y.; Lin,W.; Dyck,J.A.; Yeakley,J.M.; Songyang,Z.; Cantley,L.C.; Fu,X.D.  
 TITLE (TI): SRPK2: a differentially expressed SR protein-specific kinase involved in mediating the interaction and localization of pre-mRNA splicing factors in mammalian cells  
 JOURNAL (SO): J. Cell Biol., 140 (4), 737-750 (1998)  
 OTHER SOURCE (OS): CA 128:306636  
 REFERENCE: 42 (bases 38805 to 39836)  
 AUTHOR (AU): Frodyma,M.E.; Downs,D.  
 TITLE (TI): ApbA, the ketopantoate reductase enzyme of *Salmonella typhimurium* is required for the synthesis of thiamine via the alternative pyrimidine biosynthetic pathway  
 JOURNAL (SO): J. Biol. Chem., 273 (10), 5572-5576 (1998)  
 OTHER SOURCE (OS): CA 128:305459  
 REFERENCE: 43 (bases 106231 to 106803)  
 AUTHOR (AU): Woloshuk,C.P.; Prieto,R.  
 TITLE (TI): Genetic organization and function of the aflatoxin B1 biosynthetic genes  
 JOURNAL (SO): FEMS Microbiol. Lett., 160 (2), 169-176 (1998)  
 OTHER SOURCE (OS): CA 128:290649  
 REFERENCE: 44 (bases 93571 to 94963)  
 AUTHOR (AU): Philp,N.J.; Yoon,H.; Grollman,E.F.  
 TITLE (TI): Monocarboxylate transporter MCT1 is located in the apical membrane and MCT3 in the basal membrane of rat RPE  
 JOURNAL (SO): Am. J. Physiol., 274 (6 PT 2), R1824-R1828 (1998)  
 OTHER SOURCE (OS): CA 129:159493  
 REFERENCE: 45 (bases 93571 to 94963)

AUTHOR (AU): Wilson,M.C.; Jackson,V.N.; Heddle,C.; Price,N.T.;  
Pilegaard,H.; Juel,C.; Bonen,A.; Montgomery,I.;  
Hutter,O.F.; Halestrap,A.P.

TITLE (TI): Lactic acid efflux from white skeletal muscle is  
catalyzed by the monocarboxylate transporter isoform  
MCT3

JOURNAL (SO): J. Biol. Chem., 273 (26), 15920-15926 (1998)

OTHER SOURCE (OS): CA 129:159801

REFERENCE: 46 (bases 153410 to 154508)

AUTHOR (AU): Dekkers,L.C.; van der Bij,A.J.; Mulders,I.H.;  
Phoelich,C.C.; Wentwoord,R.A.; Glandorf,D.C.;  
Wijffelman,C.A.; Lugtenberg,B.J.

TITLE (TI): Role of the O-antigen of lipopolysaccharide, and  
possible roles of growth rate and of NADH:ubiquinone  
oxidoreductase (nuo) in competitive tomato root-tip  
colonization by *Pseudomonas fluorescens* WCS365

JOURNAL (SO): Mol. Plant Microbe Interact., 11 (8), 763-771 (1998)

OTHER SOURCE (OS): CA 129:200426

REFERENCE: 47 (bases 146433 to 148685)

AUTHOR (AU): Saito,K.; Yamazaki,H.; Ohnishi,Y.; Fujimoto,S.;  
Takahashi,E.; Horinouchi,S.

TITLE (TI): Production of trehalose synthase from a basidiomycete,  
*Grifola frondosa*, in *Escherichia coli*

JOURNAL (SO): Appl. Microbiol. Biotechnol., 50 (2), 193-198 (1998)

OTHER SOURCE (OS): CA 130:956

REFERENCE: 48 (bases 122486 to 123895)

AUTHOR (AU): Kimura,M.; Matsumoto,G.; Shingu,Y.; Yoneyama,K.;  
Yamaguchi,I.

TITLE (TI): The mystery of the trichothecene 3-O-acetyltransferase  
gene. Analysis of the region around Tri101 and  
characterization of its homologue from *Fusarium*  
*sporotrichioides*

JOURNAL (SO): FEBS Lett., 435 (2-3), 163-168 (1998)

OTHER SOURCE (OS): CA 130:11163

REFERENCE: 49 (bases 146433 to 148685)

AUTHOR (AU): Saito,K.; Kase,T.; Takahashi,E.; Horinouchi,S.

TITLE (TI): Purification and characterization of a trehalose  
synthase from the basidiomycete *grifola frondosa*

JOURNAL (SO): Appl. Environ. Microbiol., 64 (11), 4340-4345 (1998)

OTHER SOURCE (OS): CA 130:34870

REFERENCE: 50 (bases 14029 to 15172)

AUTHOR (AU): Feng,Y.; Khoo,H.E.; Poh,C.L.

TITLE (TI): Purification and characterization of gentisate  
1,2-dioxygenases from *Pseudomonas alcaligenes* NCIB 9867  
and *Pseudomonas putida* NCIB 9869

JOURNAL (SO): Appl. Environ. Microbiol., 65 (3), 946-950 (1999)

OTHER SOURCE (OS): CA 130:322223

REFERENCE: 51 (bases 59070 to 60560)

AUTHOR (AU): Bosch,R.; Moore,E.R.; Garcia-Valdes,E.; Pieper,D.H.

TITLE (TI): NahW, a novel, inducible salicylate hydroxylase  
involved in mineralization of naphthalene by  
*Pseudomonas stutzeri* AN10

JOURNAL (SO): J. Bacteriol., 181 (8), 2315-2322 (1999)

OTHER SOURCE (OS): CA 131:70144

REFERENCE: 52

AUTHOR (AU): DeZwaan,T.M.; Carroll,A.M.; Valent,B.; Sweigard,J.A.

TITLE (TI): *Magnaporthe grisea* pth11p is a novel plasma membrane  
protein that mediates appressorium differentiation in  
response to inductive substrate cues

JOURNAL (SO): Plant Cell, 11 (10), 2013-2030 (1999)

OTHER SOURCE (OS): CA 132:47358

REFERENCE: 53 (bases 122486 to 123895)

AUTHOR (AU): McCormick, S.P.; Alexander, N.J.; Trapp, S.E.; Hohn, T.M.  
 TITLE (TI): Disruption of TRI101, the gene encoding trichothecene 3-O-acetyltransferase, from *Fusarium sporotrichioides*  
 JOURNAL (SO): Appl. Environ. Microbiol., 65 (12), 5252-5256 (1999)  
 OTHER SOURCE (OS): CA 132:118174  
 REFERENCE: 54 (bases 111907 to 113460)  
 AUTHOR (AU): Muraguchi, H.; Kamada, T.  
 TITLE (TI): A mutation in the *eln2* gene encoding a cytochrome P450 of *Coprinus cinereus* affects mushroom morphogenesis  
 JOURNAL (SO): Fungal Genet. Biol., 29 (1), 49-59 (2000)  
 OTHER SOURCE (OS): CA 134:96073  
 REFERENCE: 55 (bases 108826 to 111209)  
 AUTHOR (AU): Yu, J.; Chang, P.K.; Bhatnagar, D.; Cleveland, T.E.  
 TITLE (TI): Genes encoding cytochrome P450 and monooxygenase enzymes define one end of the aflatoxin pathway gene cluster in *Aspergillus parasiticus*  
 JOURNAL (SO): Appl. Microbiol. Biotechnol., 53 (5), 583-590 (2000)  
 OTHER SOURCE (OS): CA 133:291807  
 REFERENCE: 56 (bases 122486 to 123895)  
 AUTHOR (AU): Muhitch, M.J.; McCormick, S.P.; Alexander, N.J.; Hohn, T.M.  
 TITLE (TI): Transgenic expression of the TRI101 or PDR5 gene increases resistance of tobacco to the phytotoxic effects of the trichothecene 4,15-diacetoxyscirpenol  
 JOURNAL (SO): Plant Sci., 157 (2), 201-207 (2000)  
 OTHER SOURCE (OS): CA 133:306551  
 REFERENCE: 57 (bases 107279 to 108340)  
 AUTHOR (AU): Cheng, Q.; Thomas, S.M.; Kostichka, K.; Valentine, J.R.; Nagarajan, V.  
 TITLE (TI): Genetic analysis of a gene cluster for cyclohexanol oxidation in *Acinetobacter* sp. Strain SE19 by in vitro transposition  
 JOURNAL (SO): J. Bacteriol., 182 (17), 4744-4751 (2000)  
 OTHER SOURCE (OS): CA 134:37832  
 REFERENCE: 58 (bases 100363 to 101496)  
 AUTHOR (AU): Jornvall, H.; Hoog, J.O.; Persson, B.; Pares, X.  
 TITLE (TI): Pharmacogenetics of the alcohol dehydrogenase system  
 JOURNAL (SO): Pharmacology, 61 (3), 184-191 (2000)  
 OTHER SOURCE (OS): CA 134:38655  
 REFERENCE: 59  
 AUTHOR (AU): Calabrese, D.; Bille, J.; Sanglard, D.  
 TITLE (TI): A novel multidrug efflux transporter gene of the major facilitator superfamily from *Candida albicans* (FLU1) conferring resistance to fluconazole  
 JOURNAL (SO): Microbiology (Reading, Engl.), 146 (PT 11), 2743-2754 (2000)  
 OTHER SOURCE (OS): CA 135:1055  
 REFERENCE: 60  
 AUTHOR (AU): Deising, H.B.; Werner, S.; Wernitz, M.  
 TITLE (TI): The role of fungal appressoria in plant infection  
 JOURNAL (SO): Microbes Infect., 2 (13), 1631-1641 (2000)  
 REFERENCE: 61 (bases 43783 to 45994)  
 AUTHOR (AU): Smith, S.  
 TITLE (TI): The world according to PARP  
 JOURNAL (SO): Trends Biochem. Sci., 26 (3), 174-179 (2001)  
 OTHER SOURCE (OS): CA 135:15779  
 REFERENCE: 62 (bases 131646 to 132375)  
 AUTHOR (AU): Cronk, J.D.; Endrizzi, J.A.; Cronk, M.R.; O'Neill, J.W.; Zhang, K.Y.  
 TITLE (TI): Crystal structure of *E. coli* beta-carbonic anhydrase, an enzyme with an unusual pH-dependent activity  
 JOURNAL (SO): Protein Sci., 10 (5), 911-922 (2001)  
 REFERENCE: 63 (bases 43783 to 45994)

AUTHOR (AU): Ziegler,M.; Oei,S.L.  
 TITLE (TI): A cellular survival switch: poly(ADP-ribosyl)ation stimulates DNA repair and silences transcription  
 JOURNAL (SO): Bioessays, 23 (6), 543-548 (2001)  
 REFERENCE: 64 (bases 43783 to 45994)  
 AUTHOR (AU): Herceg,Z.; Wang,Z.Q.  
 TITLE (TI): Functions of poly(ADP-ribose) polymerase (PARP) in DNA repair, genomic integrity and cell death  
 JOURNAL (SO): Mutat. Res., 477 (1-2), 97-110 (2001)  
 OTHER SOURCE (OS): CA 136:145570  
 REFERENCE: 65 (bases 15614 to 17392)  
 AUTHOR (AU): Mundodi,S.R.; Watson,B.S.; Lopez-Meyer,M.; Paiva,N.L.  
 TITLE (TI): Functional expression and subcellular localization of the Nectria haematococca Mak1 phytoalexin detoxification enzyme in transgenic tobacco  
 JOURNAL (SO): Plant Mol. Biol., 46 (4), 421-432 (2001)  
 OTHER SOURCE (OS): CA 135:285870  
 REFERENCE: 66 (bases 1 to 163680)  
 AUTHOR (AU): Pel,H.J.; de Winde,J.H.; Archer,D.B.; Dyer,P.S.; Hofmann,G.; Schaap,P.J.; Turner,G.; de Vries,R.P.; Albang,R.; Albermann,K.; Andersen,M.R.; Bendtsen,J.D.; Benen,J.A.; van den Berg,M.; Breestraat,S.; Caddick,M.X.; Contreras,R.; Cornell,M.; Coutinho,P.M.; Danchin,E.G.; Debets,A.J.; Dekker,P.; van Dijck,P.W.; van Dijk,A.; Dijkhuizen,L.; Driessen,A.J.; d'Enfert,C.; Geysens,S.; Goosen,C.; Groot,G.S.; de Groot,P.W.; Guillemette,T.; Henrissat,B.; Herweijer,M.; van den Hombergh,J.P.; van den Hondel,C.A.; van der Heijden,R.T.; van der Kaaij,R.M.; Klis,F.M.; Kools,H.J.; Kubicek,C.P.; van Kuyk,P.A.; Lauber,J.; Lu,X.; van der Maarel,M.J.; Meulenberg,R.; Menke,H.; Mortimer,M.A.; Nielsen,J.; Oliver,S.G.; Olsthoorn,M.; Pal,K.; van Peij,N.N.; Ram,A.F.; Rinas,U.; Roubos,J.A.; Sagt,C.M.; Schmoll,M.; Sun,J.; Ussery,D.; Varga,J.; Vervecken,W.; van de Vondervoort,P.J.; Wedler,H.; Wosten,H.A.; Zeng,A.P.; van Ooyen,A.J.; Visser,J.; Stam,H.  
 TITLE (TI): Genome sequencing and analysis of the versatile cell factory *Aspergillus niger* CBS 513.88  
 JOURNAL (SO): Nat. Biotechnol., 25 (2), 221-231 (2007)  
 OTHER SOURCE (OS): CA 146:310276  
 REFERENCE: 67 (bases 1 to 163680)  
 AUTHOR (AU): Pel,H.J.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (01-MAY-2006) Pel H.J., DSM, 624-0295, P.O. Box 1, 2600 MA Delft, THE NETHERLANDS

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		sequence:UniProtKB:AE010349.4"
		/note="unnamed protein product;
		Title: weak similarity to
		hypothetical acetyltransferase
		MK0549 - Methanopyrus kandle"
		/codon-start=1
		/protein-id="CAK47172.1"
		/db-xref="GI:134084139"
		/translation="MTKSQFEVREIHTKEEYARL
		VDVLWSANFNPNPVFTAVHPVSG
		HTAEDRVKDKALDTEIRWAAHEKNPASHLIYVID
		TETGRVAGGCEWLIFHKNPFPNGP
		QPLSCTWYPEGSERAHEYASRMLSQAFFPRMCWLQ
		RPHAGVNAMGVHPDYRRRGVGRLL
		MQWGHHERIDPLGYESWIEGSPIGRWLYEESGYKR
		VISLNIDFAKKNPSDEWNRLVHEC
		QPPAILLLWRPPRGEWNDKVPPGPWAVTEDTWK"
exon	complement(3788..4122)	/locus-tag="An18g00950"
intron	complement(4123..4200)	/number=1 /locus-tag="An18g00950"
exon	complement(4201..4523)	/number=1 /locus-tag="An18g00950"
intron	complement(4524..4677)	/number=2 /locus-tag="An18g00950"
exon	complement(4678..4775)	/number=2 /locus-tag="An18g00950"
gene	complement(<5212..>7379)	/number=3 /locus-tag="An18g00960"
mRNA	complement(join(<5212..5456,5493..5664,5746..6075,6140..6159,6225..6602,6674..6746,6800..6899,7249..>7379))	/locus-tag="An18g00960"
CDS	complement(join(5212..5456,5493..5664,5746..6075,6140..6159,6225..6602,6674..6746,6800..6899,7249..7379))	/locus-tag="An18g00960"

456,5493..5664,  
5746..6075,6140..6159,  
6225..6602,6674..6746,  
6800..6899,7249..7379))

/inference="profile:COGS:COG0833"  
/inference="similar to AA  
sequence:PIR:S11175"  
/note="unnamed protein product;  
Function: Hnml of *S. cerevisiae* is  
the unique coline permease in  
yeast (Km of 0.5 micromolar).  
Regulation: in *S. cerevisiae*,  
expression of HNML gene is  
regulated by the phospholipid  
precursors inositol and choline  
and this regulation involves the  
trans-acting factors Ino2p, Ino4p  
and Opilp. Remark: alternate name  
for *S. cerevisiae* Hnml is YGL077c.  
Similarity: Hnml of *S. cerevisiae*  
belongs to the APC family, which  
encompasses amino acid permeases  
more related to the mammalian  
cationic amino-acid transporter  
family (Tea/ecoR). Title: strong  
similarity to choline permease  
Hnml -*Saccharomyces cerevisiae*  
plasma membrane"  
/citation=[12]  
/citation=[19]  
/citation=[24]  
/codon-start=1  
/protein-id="CAK47173.1"  
/db-xref="GI:134084140"  
/translation="MARNSDVEHSIELRAPTNRD  
SGTPSKATFSDDAYELARVGKKEV  
GGPAGLVYGFGLGVWAGIISVFISMGELASMMPSA  
GGQYHWVSILAPRSARKFLSHVTG  
SVCIIAWTAAPTAAIYLAASVLQSTIAMNIPSYD  
PKGWHITLIMWAILLVCTVLNTWL  
GMILPVIEVLILLVHVLGFFAVLVPLVYLGPKAD  
PRSIFTVSFDYGGWGDLTATFIG  
LKGTVAAFVGTGDGAVHMAEEVANSSRVVPRSMML  
ALMINGATGFALIAFLFTAGDLL  
KIVESSASYPFMYMLASSTGSKGAAVVLSSMMAI  
LQACAGLAGISSGSRMLWSFSREQ  
AIPGWRWRVQVNQRTLVPFHSTLVVVVAAGLLSL  
INIGSAVVLNIIILSLVLEAFFASY  
MISLTLLLYRGGVLNWGPFRVKGWLGTANNIFAI  
AYSIIIMFFGCWPPENHPAPKNIN  
YSIVIFAGVTLISIIYYVGWARKHYQGPLAEL"

exon	complement(5212..5456)	/locus-tag="An18g00960" /number=1
intron	complement(5457..5492)	/locus-tag="An18g00960" /number=1
exon	complement(5493..5664)	/locus-tag="An18g00960" /number=2
intron	complement(5665..5745)	/locus-tag="An18g00960" /number=2
exon	complement(5746..6075)	/locus-tag="An18g00960" /number=3
intron	complement(6076..6139)	/locus-tag="An18g00960"

exon	complement(6140..6159)	/number=3 /locus-tag="An18g00960"
intron	complement(6160..6224)	/number=4 /locus-tag="An18g00960"
exon	complement(6225..6602)	/number=4 /locus-tag="An18g00960"
intron	complement(6603..6673)	/number=5 /locus-tag="An18g00960"
exon	complement(6674..6746)	/number=5 /locus-tag="An18g00960"
intron	complement(6747..6799)	/number=6 /locus-tag="An18g00960"
exon	complement(6800..6899)	/number=6 /locus-tag="An18g00960"
intron	complement(6900..7248)	/number=7 /locus-tag="An18g00960"
exon	complement(7249..7379)	/number=7 /locus-tag="An18g00960"
gene	complement(<7770..>8415	/number=8 /locus-tag="An18g00970"
mRNA	) complement(join(<7770.. 8282,8380..>8415))	/locus-tag="An18g00970"
CDS	complement(join(7770..8 282,8380..8415))	/locus-tag="An18g00970"
		/note="unnamed protein product; Title: weak similarity to hypothetical protein BAA96207.1 - Oryza sativa" /codon-start=1 /protein-id="CAK47174.1" /db-xref="GI:134084141" /translation="MLCTHAGGEGARSGRPDDRQ GHQPISVALWLCAPPPGFLSGRTS LASAGISNPDGATAVNTCETVGCLGLTACGQDCL SSRAALAEALLLGLCCVGDGGGRA PANPNKMDRYLLLYCRLGLTLDGPIVVVVVHTLS LSCSPPTQLHPPPLLASLHSFFPP ESLGRVPISIIYAHMRHAAAKIV"
exon	complement(7770..8282)	/locus-tag="An18g00970"
intron	complement(8283..8379)	/number=1 /locus-tag="An18g00970"
exon	complement(8380..8415)	/number=1 /locus-tag="An18g00970"
gene	<8621..>9700	/number=2 /locus-tag="An18g00980"
mRNA	join(<8621..8764, 8830..9156,9214..9356, 9406..>9700)	/locus-tag="An18g00980"
CDS	join(8621..8764, 8830..9156,9214..9356, 9406..9700)	/locus-tag="An18g00980"
		/note="unnamed protein product; Function: M. grisea Pth11 is a pathogenicity gene. Function: M. grisea Pth11p is likely to be involved in host surface recognition. Function: M. grisea pth11 mutants of strain 4091-5-8 are nonpathogenic due to a defect in appressorium differentiation. Localization: in M. grisea, a

Pth11-green fluorescent protein fusion localised to the cell membrane and vacuoles. Similarity: similarity of the predicted A. niger protein and M. grisea Pth11 is limited to the N-terminal half of the protein sequences. Title: weak similarity to integral membrane protein PTH11 - Magnaporthe grisea plasma membrane"

/citation=[52]  
/codon-start=1  
/protein-id="CAK47175.1"  
/db-xref="GI:134084142"  
/translation="MTDHSAAVKVVTCTLLIVSF  
IAVVACLTNNQVLRKVSSVALL  
LSTLIASIASGAAVSVAATHGLGQASPLTDAQVV  
VMQKALYSMEVLYVLTGLGLKLSV  
MVLFYSLSSSTGQSKSVLAATGLLLIWWVVMVIV  
VCLQCHPPEVWNIVGGTCLDLGI  
WIAFGVMNVLVEIMIIAVPSFIIIFRLKLSLKRRL  
VVISCFGIRILDIAGSIVQLCYVR  
NFKIHADSPMPTNVWQWAICSQVLQTVAILSACV  
PYLREFLESFPGMFKPTCLKHPT  
VQSAYNATKCSDSIELMRPESTKDT"

sig-peptide 8621..8698 /locus-tag="An18g00980"  
/inference="protein  
motif:SignalP:2.0"

mat-peptide join(8699..8764,  
8830..9156,9214..9356,  
9406..9697) /locus-tag="An18g00980"

exon 8621..8764 /product="unnamed"  
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/number=1

intron 8765..8829 /locus-tag="An18g00980"  
/number=1

exon 8830..9156 /locus-tag="An18g00980"  
/number=2

intron 9157..9213 /locus-tag="An18g00980"  
/number=2

exon 9214..9356 /locus-tag="An18g00980"  
/number=3

intron 9357..9405 /locus-tag="An18g00980"  
/number=3

exon 9406..9700 /locus-tag="An18g00980"  
/number=4

gene complement(<9787..>9927 /locus-tag="An18g00990"  
)

mRNA complement(<9787..>9927 /locus-tag="An18g00990"  
)

CDS complement(9787..9927) /locus-tag="An18g00990"  
/note="unnamed protein product;  
Title: strong similarity to EST  
an-1359 -Aspergillus niger"  
/codon-start=1  
/protein-id="CAK47176.1"  
/db-xref="GI:134084143"  
/translation="MRAATLLLVALSAVALALPT  
TNNVERAAADANVRQMDELTVAAI SK"

sig-peptide complement(9877..9927) /locus-tag="An18g00990"  
/inference="protein"

mat-peptide	complement(9790..9876)	motif:SignalP:2.0" /locus-tag="An18g00990" /product="unnamed"
exon	complement(9787..9927)	/locus-tag="An18g00990" /number=1
gene	<10500..>11479	/locus-tag="An18g01000"
mRNA	join(<10500..10749, 10812..11041, 11105..>11479)	/locus-tag="An18g01000"
CDS	join(10500..10749, 10812..11041, 11105..11479)	/locus-tag="An18g01000"  /note="unnamed protein product; Similarity: the nucleotide sequence of the ORF shows strong similarity to the ESTs an-2192 and an-2204 of A. niger. Title: strong similarity to EST an-2192 -Aspergillus niger" /codon-start=1 /protein-id="CAK47177.1" /db-xref="GI:134084144" /translation="MYSYEKVNRRDDSDQGLLAE DSERVAPQPRVSRFPSWTNALLLL GLLFSLSLNVGWVFVQKGHNVP IQDLDPDAAMAK QRSPYTGLAWDTHKPYSHHSEYTS ENATHADEMWESLSMDPMVIAPTWEWAQSKGLSD SWAFPWDSNRRIYFIKVFHQLHCL KLMRHSYHELWSGQESSIPAPHIEHCLDSL RQDL MCKADDTMPPSLQLLNGGGEGQQM QCKDFDKLVAWSKAPERNACYKRLTDYKPIVHSI ERYAFCPEDSEHYPTMSKYFEEHG HYADPFSE"
exon	10500..10749	/locus-tag="An18g01000" /number=1
intron	10750..10811	/locus-tag="An18g01000" /number=1
exon	10812..11041	/locus-tag="An18g01000" /number=2
intron	11042..11104	/locus-tag="An18g01000" /number=2
exon	11105..11479	/locus-tag="An18g01000" /number=3
gene	<11980..>13464	/locus-tag="An18g01010"
mRNA	join(<11980..12137, 12198..>13464)	/locus-tag="An18g01010"
CDS	join(11980..12137, 12198..13464)	/locus-tag="An18g01010"  /inference="profile:COGS:COG0477" /note="unnamed protein product; Function: FLU1 of C. albicans facilitates resistance to fluconazole and cycloheximide in the fluconazole-hypersensitive S. cerevisiae strain YKKB-13 lacking the ABC (ATP-binding cassette) transporter gene PDR5. Function: FLU1 of C. albicans facilitates resistance to mycophenolic acid in C. albicans. Function: FLU1 of C. albicans is involved in the resistance to azol derivatives in C. albicans. Function: MDR1 of C.

albicans facilitates resistance to the anti-mitotic drug benomyl and to the dihydrofolate reductase inhibitor methotrexate. Similarity: N-terminus of the A. niger protein is app. 120 aa shorter than in FLU1 of C. albicans. Similarity: the predicted A. niger protein shows strong similarity to fluconazole resistance protein FLU1 of C. albicans, which is a permease belonging to the major facilitator superfamily. Title: strong similarity to fluconazole resistance protein FLU1 - Candida albicans"

/citation=[59]  
/codon-start=1  
/protein-id="CAK47178.1"  
/db-xref="GI:134084145"  
/translation="MDEEDGHCKETEVTVQSTSP  
VDSADYDPFDPQTRSTTYKWITVV  
LVAGLSTMVQLSTIIAAPVSPSILAHFHS DNALY  
RTLIVSIWELGEIVAPLLWGPLSE  
LYGRQWPLNIANLFFVAFLAGTAASTSIQMLIAF  
RFLSGAATAASAIGPGIVSDLFPE  
ESRGRAMSIMSLTGALGPVVGPIIGSYLGEKAGW  
RWAFLPTIATGTLSLLILVVYRE  
TYSVTLQKRKARQQNPESGSKSPEDTDKTASQVF  
FKAILRPLRLLIRSPMLILVTFYL  
SVVYGYTYLVMTTIAPLFQDVYGFSEGLAFL  
GLCLGLILGAFLCSFLLDRYVRTA  
RARSGTSKPEQRLPPVLIACFVMSGGLFLFGWTA  
QYHVQWIAPIIGTGIIGFLVSTT  
ITLQTYVVDLFGIYAASATSAMLVPRNACAAFLP  
LAGPPLFDRLGYNWGGTLLALIVL  
VFSLMPLIFINYGERLRGKNLLDD"

/locus-tag="An18g01010"  
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/locus-tag="An18g01010"  
/number=1

/locus-tag="An18g01010"  
/number=2

/locus-tag="An18g01020"

/locus-tag="An18g01020"

/locus-tag="An18g01020"

/EC-number="1.13.11.4"  
/inference="profile:COGS:COG3435"  
/inference="similar to AA  
sequence:UniProtKB:AF173167.3"  
/note="unnamed protein product;  
Complex: the estimated molecular  
mass of the purified gentisate 1,  
2-dioxygenase of P. alcaligenes  
was 154 kDa, with a subunit mass  
of 39 kDa. its structure is

exon 11980..12137

intron 12138..12197

exon 12198..13464

gene complement(<14029..>15172)

mRNA complement(join(<14029..14318,14411..14845,14917..>15172))

CDS complement(join(14029..14318,14411..14845,14917..15172))

deduced to be a tetramer. Remark:  
 gentisate 1,2-dioxygenase of *P. alcaligenes* exhibits typical  
 saturation kinetics and has an  
 apparent  $K_m$  of 92  $\mu\text{M}$  for  
 gentisate. this enzyme has broad  
 substrate specificities towards  
 alkyl and halogenated gentisate  
 analogs. Similarity: the predicted  
*A. niger* protein shows strong  
 similarity to gentisate  
 1,2-dioxygenase of *P. alcaligenes*  
 and conserved hypothetical  
 proteins from other procaryotic  
 species. Title: strong similarity  
 to gentisate 1,2-dioxygenases xlnE  
 - *Pseudomonas alcaligenes*"  
 /citation=[50]  
 /codon-start=1  
 /protein-id="CAK47179.1"  
 /db-xref="GI:134084146"  
 /translation="MSPSACNTGSGNGADSAEQLL  
 QDLKKSNTLPLWTQMTRLNPPEPN  
 PTAVPFIWRYDSIRPNLLRAGELVTEKQAERRVL  
 MLVNPARDAPYTTDTLYAGLQLVM  
 PNETAPAHRHTAFAMRYIIIEGNGGFTAVHGKRIK  
 MQKGDVILTPTWNYHDHGKDGTTGP  
 MIWLDGLDLPNFRHFPVHFVDHYDQPRYPADVD  
 SATSPIVFPWDKMKAEKDKAPGTW  
 AVRRYL RADGSEGGSAERVDAGTSSLPRQET TSA  
 VYHVIAGSGCSEIGDKTLVWETGD  
 TFCVPSWYKYRHIAAEGETVYLYRFDDKPMISAL  
 GFYRSIDTDLATLVSQ"

exon	complement(14029..14318 )	/locus-tag="An18g01020" /number=1
intron	complement(14319..14410 )	/locus-tag="An18g01020" /number=1
exon	complement(14411..14845 )	/locus-tag="An18g01020" /number=2
intron	complement(14846..14916 )	/locus-tag="An18g01020" /number=2
exon	complement(14917..15172 )	/locus-tag="An18g01020" /number=3
gene	<15614..>17392	/locus-tag="An18g01030"
mRNA	join(<15614..15661, 15723..16281, 16347..16503, 16584..16739, 16803..16942, 17034..>17392)	/locus-tag="An18g01030"
CDS	join(15614..15661, 15723..16281, 16347..16503, 16584..16739, 16803..16942, 17034..17392)	/locus-tag="An18g01030"  /inference="profile:COGS:COG0654"

/inference="profile:PFAM:PF01360"  
 /note="unnamed protein product;  
 Function: Mak1 from N.  
 haematococca specifically  
 hydroxylates the phytoalexins  
 medicarpin and  
 maackiain, converting them to less  
 fungitoxic derivatives.  
 Localization: heterologous  
 expression of the Mak1 cDNA  
 construct in plants indicated that  
 Mak1 protein accumulates in the  
 plant cytoplasm, associated with  
 endoplasmic reticulum membranes.  
 Similarity: the predicted A. niger  
 protein shows strong similarity to  
 Mak1 from the fungal pathogen N.  
 haematococca. Mak1 belongs to the  
 flavin-containing mono-oxygenases.  
 best matches are with putative  
 salicylate hydroxylases of several  
 procaryotic species. Title: strong  
 similarity to maackiain  
 detoxification protein 1 MAK1 -  
 Nectria haematococca endoplasmatic  
 reticulum"  
 /citation=[31]  
 /citation=[65]  
 /codon-start=1  
 /protein-id="CAK47180.1"  
 /db-xref="GI:134084147"  
 /translation="MASTRMSAQSTIADLRVPDY  
 PSNCLQFTQQLTASATHLTPQKDA  
 SVRLNIILAGAGLGGLATAIALAQAGHAVKIYEQ  
 TPVLGEVGAGIQIPSNSTRILFSL  
 GLQSYLEPYVTAPESISFRRWQNGKVI GLTKLIP  
 NFVNNFKAPYYVIHRADFHSALCQ  
 KALDVGVEIELGAKVVDYDPIVGSITLADGTHKS  
 ADLIVAADGIKSVARNVVLQGDEM  
 RFQGPFGFAAYRAVVDVGKMRRDPDL SWILEKPAL  
 NIWIGDSRHVMTYTIGAGKAFNMV  
 LSHPEMTDPGTWKPETALEDMKAEFQGWDPILSK  
 IIGMVEKTVKWPLLTGTLLQNWTV  
 GKLVI LGDAAHAMVPYMSQGAAMAVEDGIALSRS  
 LSHMSTRDQLQKALSIFQEVRRKR  
 AGHMQEASLLNGKLWHFPDGSLLQARDEAMAPEV  
 QGIPF SHSPNQWSDPATQMWCYGY  
 DAEAAIDIAWMESLEARVDCVH"  
 /locus-tag="An18g01030"  
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 /locus-tag="An18g01030"  
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 /locus-tag="An18g01030"  
 /number=2  
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 /locus-tag="An18g01030"  
 /number=3  
 /locus-tag="An18g01030"  
 /number=3  
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 /number=4

exon	15614..15661
intron	15662..15722
exon	15723..16281
intron	16282..16346
exon	16347..16503
intron	16504..16583
exon	16584..16739



intron	16740..16802	/locus-tag="An18g01030"
		/number=4
exon	16803..16942	/locus-tag="An18g01030"
		/number=5
intron	16943..17033	/locus-tag="An18g01030"
		/number=5
exon	17034..17392	/locus-tag="An18g01030"
		/number=6
gene	<17766..>20491	/locus-tag="An18g01040"
mRNA	join(<17766..17864, 17939..18039, 18108..18343, 18398..19163, 19373..19935, 20037..20252, 20325..>20491)	/locus-tag="An18g01040"
CDS	join(17766..17864, 17939..18039, 18108..18343, 18398..19163, 19373..19935, 20037..20252, 20325..20491)	

/inference="profile:PFAM:PF00172"  
 /inference="similar to AA  
 sequence:UniProtKB:ENU56097.1"  
 /note="unnamed protein product;  
 Phenotype: facB recessive loss of  
 function mutants in A. nidulans  
 are deficient in acetate induction  
 of acetyl-CoA synthase, isocitrate  
 lyase, malate  
 synthase, acetamidase, and  
 NADP-isocitrate dehydrogenase.  
 Similarity: the predicted A. niger  
 protein shows similarity to  
 acetate regulatory DNA binding  
 protein FacB (facB) from A.  
 nidulans, which belongs to the  
 GAL4-type zinc cluster  
 transcriptional activators. Title:  
 similarity to acetate regulatory  
 DNA binding protein facB -  
 Aspergillus nidulans"  
 /citation=[37]  
 /codon-start=1  
 /protein-id="CAK47181.1"  
 /db-xref="GI:134084148"  
 /translation="MDFAPELPTPQGQSVKRRRV  
 ALACDACRTRKSRCDGRRPKCGMC  
 EDLGFECAYTPSTTTTNIIVQKDYLRDLEERVKS  
 LETSMATVKSDLGSGFASQINGSMP  
 DAPRKENPLSNQSERFSDFAGTEDTIDAMGAVAF  
 ADEEDCGFFGPSSNIAFLRHLSCA  
 VAHSASAQKEITSPPLDRVAYDGGFVSATRPSSP  
 SHDQRPESELEGEKFDKFALPPPEE  
 SLALIHRYFADTGLLFPYIHPPTFFETYAELKDN  
 SKRVRRTWLGLLNIIILAMAKLTAV  
 SGT TSAETGISESAIYYHRALSLCKGEILRGTTL  
 EVGRYSIYAPVRARVPVYL RATKI  
 NTVQYLLVMGQYLGQTQKSVQAWTIHGLAVKAAL  
 QLGLHSGASRAFTPLEQEVRKRT

		WFGCVVLDVRANLFLNKRKTIQQANIRVSTLYK QIANIIDRIYGQNLGCDSPLSIGE TVGRVLGIENQLFSWVLGLPESLRQVTVQSMREE IERSEVGDEGHHKLYPLKFRIILT LRYFHVQILLHRPILVKFLDATGPSGLEADEVKL LNDIGYSSMNKCVDSAMGIIDIIH ELVSTTGWQKDLLGAWWYSLYYTFNAALVIIGAM WVQRNRDTSEDPVDNGGNNNNMDI YLSRAVLTLQNLNVGNRMVDRCKYYLDQLITLLG LQADRIAETGIIISGMNPNVAGNST TGFDFPSLGIECGEFMIDDFPGFARGSGFERW"
exon	17766..17864	/locus-tag="An18g01040"
		/number=1
intron	17865..17938	/locus-tag="An18g01040"
		/number=1
exon	17939..18039	/locus-tag="An18g01040"
		/number=2
intron	18040..18107	/locus-tag="An18g01040"
		/number=2
exon	18108..18343	/locus-tag="An18g01040"
		/number=3
intron	18344..18397	/locus-tag="An18g01040"
		/number=3
exon	18398..19163	/locus-tag="An18g01040"
		/number=4
intron	19164..19372	/locus-tag="An18g01040"
		/number=4
exon	19373..19935	/locus-tag="An18g01040"
		/number=5
intron	19936..20036	/locus-tag="An18g01040"
		/number=5
exon	20037..20252	/locus-tag="An18g01040"
		/number=6
intron	20253..20324	/locus-tag="An18g01040"
		/number=6
exon	20325..20491	/locus-tag="An18g01040"
		/number=7
gene	complement(<20773..>22555)	/locus-tag="An18g01050"
mRNA	complement(join(<20773..21444,21501..21638,21710..22119,22180..22303,22370..>22555))	/locus-tag="An18g01050"
CDS	complement(join(20773..21444,21501..21638,21710..22119,22180..22303,22370..22555))	/locus-tag="An18g01050"

/EC-number="1.13.11.43"  
 /inference="profile:COGS:COG3670"  
 /inference="profile:PFAM:PF03055"  
 /inference="similar to AA  
 sequence:PIR:JC4324"  
 /note="unnamed protein product;  
 Catalytic activity:  
 lignostilbene-alpha,beta-dioxygena  
 se isozymes (LSD-I, II, and III)  
 of P. paucimobilis catalyze the  
 reaction  
 1,2-bis(4-hydroxy-3-methoxyphenyl)  
 ethylene + O(2) = 2 vanillin

Cofactor:  
lignostilbene-alpha,beta-dioxygena  
se isozymes (LSD-I, II, and III)  
of *P. paucimobilis* require iron as  
a cofactor. Complex: LSD-I, II,  
and III consist of alpha  
alpha,alpha beta, and beta beta  
subunits, respectively. they show  
different specificities for  
several substrates that are  
stilbene and styrene derivatives.  
Function: LSD of *P. paucimobilis*  
catalyses the oxidative cleavage  
of the interphenyl double bond in  
the synthetic substrate and  
lignin-derived stilbenes. it is  
responsible for the degradation of  
a diarylpropane-type structure in  
lignin. Similarity: the predicted  
*A. niger* protein shows strong  
similarity to subunit lsdB of  
lignostilbene-alpha,beta-dioxygena  
se isozyme LSD-III of *P.*  
*paucimobilis* and related  
dioxygenases from several plant  
species. Title: strong similarity  
to subunit lsdB of  
lignostilbene-alpha,beta-dioxygena  
se isozyme LSD-III -*Pseudomonas*  
*paucimobilis*"  
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RRGAKTADVKKWFQYKNSFPGHTANAHEDSSGNLI  
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SSIRSQLVRFTINPRAEDLNLTEPRILQADNSEF  
YRIDDRYATKPHRHVFFDMMDPSL  
GTDFARIAPVLGGGYPLYNSLARFDNVTGETEVY  
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		5-carboxymethyl-2-hydroxymuconate
		delta-isomerase from E. coli
		catalyses the reaction
		5-carboxymethyl-2-hydroxymuconate
		= 5-carboxy-2-oxohept-3-enedioate.
		Pathway:
		5-carboxymethyl-2-hydroxymuconate
		delta-isomerase from E. coli is
		involved in tyrosine and
		phenylalanine metabolism.
		Similarity: the predicted A. niger
		protein shows strong similarity to
		5-carboxymethyl-2-hydroxymuconate
		delta-isomerase from E. coli and
		many putative
		2-hydroxyhepta-2,4-diene-1,
		7-dioate isomerases from several
		procaryotic and eucaryotic
		organisms. Title: strong
		similarity to
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		delta-isomerase -Escherichia coli
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		PFPFIFFKPNTCVHDHGEPVVIPRIAQNDQADYE

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intron	23572..23666	/locus-tag="An18g01060" /number=2
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mRNA	join(<24984..25058, 25166..25301, 25564..25745, 25812..26003, 26080..26144, 26206..26646, 26722..27303, 27423..>27426)	/locus-tag="An18g01070"
CDS	join(24984..25058, 25166..25301, 25564..25745, 25812..26003, 26080..26144, 26206..26646, 26722..27303, 27423..27426)	/locus-tag="An18g01070"

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/note="unnamed protein product;  
Function: FLU1 of C. albicans facilitates resistance to fluconazole and cycloheximide in the fluconazole-hypersensitive S. cerevisiae strain YKKB-13 lacking the ABC (ATP-binding cassette) transporter gene PDR5. Function: FLU1 of C. albicans facilitates resistance to mycophenolic acid in C. albicans. Function: FLU1 of C. albicans is involved in the resistance to azol derivatives in C. albicans. Function: MDR1 of C. albicans facilitates resistance to the anti-mitotic drug benomyl and to the dihydrofolate reductase inhibitor methotrexate. Similarity: N-terminus of the A. niger protein is app. 120 aa shorter than in FLU1 of C. albicans. Similarity: the predicted A. niger protein shows strong similarity to fluconazole resistance protein FLU1 of C. albicans, which is a permease belonging to the major facilitator superfamily. Title: similarity to fluconazole resistance protein

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 MLLQAGALVWCAVATGYDSLGLGARCVLGFAAAAG  
 ESIVPEIVADIFFVHERATMMAIY  
 VVLISGGSVAVGLIGGFVMEYASGTWRSYMWLCF  
 ALASFNIVLLVFLFPESTFKRPEP  
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 NTPPFKGVLRPFHYNKDASFFKAV  
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mRNA	complement(join(<27797..28220,28259..28342,28450..28550,28602..>28667))	/locus-tag="An18g01080"
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VKSLEAGRYGHLRKHNPAAYEELNFASSNKHCCC
VMLRAYYYPRVQEEYLLRLFLYRC
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/EC-number="3.1.1.5"
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/note="unnamed protein product;
Catalytic activity:
lysophospholipase catalyses the
reaction 2-lysophosphatidylcholine
+ H(2)O = glycerophosphocholine +
a fatty acid anion. Pathway:
lysophospholipase is involved in
phospholipid degradation.
Similarity: the predicted A. niger

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protein shows strong similarity to the protein sequences lysophospholipase (sequence 5 and sequence 7) of patents WO0127251-A/5 and WO0127251-A/7 from *A. oryzae* (AC# AX112082 and AC# AX112084) and to other fungal lysophospholipases. Title: strong similarity to lysophospholipase from patent WO0127251-A - *Aspergillus oryzae* extracellular/secretion proteins"

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SGLSGGSWPAVSFPSYNFPTADEI  
VDYWKPEIDRFFTVTNTSAEAATGKAIFEQIATK  
YLAGFEVALSDYLGRGFAYEFIPG  
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PEDAEYYDLLVPSSNGTIFDLTPF  
EFGAWDGDVHAFTPTTEWLG NQLSNGIPVNQSKCW  
KGFDRSSLVIGTSADAFNFWYLES  
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DAFQETFDLNL TQISYSKFPNPFT  
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GTNLYNTYLAANATGLPFPIIPPSRTMMNLNYTL  
HPQFFGCDANLTTTGDDRPIVLY  
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intron	29876..29924	/locus-tag="An18g01090" /number=2
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31273..31630,  
31702..32218))

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/inference="profile:COGS:COG1064"  
/inference="profile:PFAM:PF00107"  
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Remark: the patent does not  
provide further information about  
the function of the protein.  
Similarity: the predicted A. niger  
protein shows strong similarity to  
the protein sequence alcohol  
dehydrogenase (sequence 19) of  
patent EP0845532-A/19 from an  
unclassified organism (AC# A92108)  
and to other zinc-containing  
dehydrogenases. Title: strong  
similarity to alcohol  
dehydrogenase from patent  
EP0845532-A - Unclassified  
organism cytoplasm"  
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SMRCTRGGVVSQVGYL GKQDPSE  
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                                GFVAENVPGANGRSIHYARGKCWGGSSAMNFMIIY
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                                ANDFLGIVGQFINMVGFNGPLTN
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		Remark: the patent does not
		provide further information about
		the function of the protein.
		Similarity: the predicted A. niger
		protein shows similarity to the
		protein fragment (SEQ ID NO:
		51484) of patent EP1033405-A2 from
		A. thaliana (AC# AAG41385) and to
		putative sterol desaturase family
		proteins. Title: similarity to
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		from patent EP1033405-A2 -
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		LIAIHQLQVMRRMGHVLGFLDGDQHGPDGVPDVG
		VAKVVRSLISTSTFRPIMTVFLSY
		RVSQAPAQMSWGWLPLEIGLYGIILDFWFYWHYHR
		LMHDVGSGLWKYHRTTHLTKHPNPL
		LTLYADTEQEFFDIAGIPLMTYFSMRLMGMPMGF
		YEWWICHQYVVFTELAGHSGLRMH
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		CVVNPLTALLDVRNGSLLANSELQEMRRQLLQEI
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CDS	join(43783..43852, 43912..44025, 44075..44344, 44395..45240, 45294..45376, 45425..45994)	/locus-tag="An18g01170"

/EC-number="2.4.2.30"  
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/note="unnamed protein product;  
Catalytic activity: the NAP  
protein of Z. mays catalyses the  
reaction NAD(+) +  
{ADP-D-ribosyl}(N)-acceptor <=>  
nicotinamide +  
{ADP-D-ribosyl}(N+1)-acceptor.  
Function: the NAP protein of Z.  
mays is involved in programmed  
cell death or apoptosis.  
Localization: the NAP protein of  
Z. mays is a nuclear enzyme.  
Remark: the ADP-D-ribosyl group of  
NAD(+) is transferred to an  
acceptor carboxyl group on a  
histone or the enzyme itself, and  
further ADP-ribosyl groups are  
transferred to the 2'-position of  
the terminal adenosine moiety,  
building up a polymer with an

average chain length of 20-30 units. Remark: the NAP polynucleotide sequences can be used for modulation of programmed cell death in eukaryotic cells. the method is used, specifically in plants, to induce, or protect against, programmed cell death, depending on the extent to which PARP activity is reduced. reducing expression of endogenous NAP class PARP only is also used to modulate programmed cell death, to increase growth rate and to produce plant cells that are more tolerant of stress (cold, chemical treatments, pathogens, pests, drought, heat, etc. , or during transformation). particular applications are generation of plants that are resistant to fungi or nematodes; are male or female sterile ; or have better seed-shatter properties. the methods are also used to improve growth of transformed plant cells (and derived calli or complete plants). Similarity: the predicted A. niger protein shows strong similarity to the protein sequence poly(ADP-ribose) polymerase NAP protein of patent WO200004173-A1 from Z. mays (AC# AAY68834) and from many other eucaryotic organisms. Title: strong similarity to poly(ADP-ribose) polymerase NAP protein from patent WO200004173-A1 - Zea mays nucleus"

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CDS	join(49850..49888, 49981..50173, 50233..50362, 50419..50614, 50702..50828, 50883..51127, 51199..51470, 51538..51919)	/locus-tag="An18g01200"
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strong similarity to  
O-methylsterigmatocystin  
(OMST)-oxidoreductase (ord1) from  
*A. flavus*, which belongs to the  
CYP64 family of cytochrome  
P450-type monooxygenases. Title:  
strong similarity to  
O-methylsterigmatocystin  
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*flavus*"

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Function: SRPK2 from M. musculus
phosphorylates SF2/ASF, a member
of SR splicing factors. Remark:
overexpression of murine SRPK2
causes disassembly of
cotransfected SF2/ASF and
endogenous SC35. SRPK family
members may regulate the
disassembly of the SR proteins in
a tissue-specific manner.
Similarity: the predicted A. niger
protein shows similarity to SRPK2
from M. musculus and strong
similarity to putative
serine/threonine protein kinases
from several eucaryotic organisms.
Title: similarity to
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Mus musculus nucleus"
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sequence:PIR:S64826"
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Function: in S. cerevisiae,
mutants (dal5) that lack
allantoate transport have been
isolated. these strains also
exhibit a 60% loss of allantoin
transport capability. Regulation:
in S. cerevisiae Dal5 appears to
be sensitive to nitrogen
catabolite repression, feedback
inhibition, and trans-inhibition.
Regulation: in S. cerevisiae
allantoate uptake is constitutive.
Similarity: the predicted A. niger
protein shows strong similarity to
allantoate permease gene (DAL5)
from S. cerevisiae, which belongs
to the major facilitator
superfamily. Title: strong
similarity to allantoate permease
Dal5 - Saccharomyces cerevisiae"
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/note="unnamed protein product;  
 Function: M. grisea Pth11 is a  
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 grisea Pth11p likely is involved  
 in host surface recognition.  
 Function: M. grisea pth11 mutants  
 of strain 4091-5-8 are  
 nonpathogenic due to a defect in  
 appressorium differentiation.  
 Localization: in M. grisea, a  
 Pth11-green fluorescent protein

fusion localised to the cell membrane and vacuoles. Similarity: similarity of the predicted A. niger protein and M. grisea Pth11 is limited to the N-terminal half of the protein sequences. Title: similarity to integral membrane protein PTH11 - Magnaporthe grisea plasma membrane"

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exon	57430..57711	/locus-tag="An18g01230"
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intron	57712..57896	/locus-tag="An18g01230"
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exon	57897..58158	/locus-tag="An18g01230"
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intron	58159..58325	/locus-tag="An18g01230"
		/number=6
exon	58326..58444	/locus-tag="An18g01230"
		/number=7
gene	<59070..>60560	/locus-tag="An18g01240"
mRNA	join(<59070..59441, 59521..59806, 59879..60178, 60237..60312,	/locus-tag="An18g01240"

CDS	60374..>60560) join(59070..59441, 59521..59806, 59879..60178, 60237..60312, 60374..60560)	/locus-tag="An18g01240"  /inference="profile:COGS:COG0654" /inference="profile:PFAM:PF01360" /note="unnamed protein product; Catalytic activity: NahW of P. stutzeri catalyzes the conversion salicylate + NADH + O(2) <=> catechol + NAD(+) + H(2)O + CO(2). Pathway: NahW of P. stutzeri is involved in the metabolization of naphtalene and salicylates (lower naphtalene degradation pathway). Similarity: the predicted A. niger protein shows similarity to salicylate hydroxylase (nahW) of P. stutzeri, which belongs to the NADH-dependent monooxygenase superfamily. Title: similarity to salicylate hydroxylase nahW -Pseudomonas stutzeri" /citation=[51] /codon-start=1 /protein-id="CAK47199.1" /db-xref="GI:134084166" /translation="MDDLPLVLIWGAGISGLLLAQ HLQKLGVPYKIFERDAAIDARSGG WGLTLHWALPALRELLPDHLVQRLPEAYVNKAAA ARGDTGRFSFFDLKTGSALYSVPA AERIRVSRVRLRQLVATGLDVQWNKTLQNIESTA DTVTAHFADGTSYTGCLLIGCDGS RSPTREILYPDSHEMNPLPVQILGAATLYTAEEM AGAAEIDPFIFQGSHPESNVFLFF SILDTPNNFVESSKDKYECQIILSWADSKDIAVP SDNGERIALMKSLASDWAEPFRTL VHRLSEDTEARSIRIADWMFRPLQNRSHPRVVL GDSAHTMTMYRGEGANNAIVDVLD LTQRVDMRSLGTMSTQALRDALDAYENDVFRRAE PSVLNSRQACVDAHDFTRILDESP LVSARVLKEDTTEQ"
sig-peptide	59070..59126	/locus-tag="An18g01240" /inference="protein motif:SignalP:2.0"
mat-peptide	join(59127..59441, 59521..59806, 59879..60178, 60237..60312, 60374..60557)	/locus-tag="An18g01240"
exon	59070..59441	/product="unnamed" /locus-tag="An18g01240"
intron	59442..59520	/number=1 /locus-tag="An18g01240"
exon	59521..59806	/number=1 /locus-tag="An18g01240"
intron	59807..59878	/number=2 /locus-tag="An18g01240"
exon	59879..60178	/number=2 /locus-tag="An18g01240"

intron	60179..60236	/number=3 /locus-tag="An18g01240"
exon	60237..60312	/number=3 /locus-tag="An18g01240"
intron	60313..60373	/number=4 /locus-tag="An18g01240"
exon	60374..60560	/number=4 /locus-tag="An18g01240"
gene	complement(<60793..>61169)	/number=5 /locus-tag="An18g01250"
mRNA	complement(join(<60793..61039,61120..>61169))	/locus-tag="An18g01250"
CDS	complement(join(60793..61039,61120..61169))	/locus-tag="An18g01250"
		/note="unnamed protein product; Title: similarity to hypothetical protein encoded by An16g00840 - Aspergillus niger" /codon-start=1 /protein-id="CAK47200.1" /db-xref="GI:134084167" /translation="MPNP SLSYGN GMSSGPKSRN VAFLTMFAVISGALLTFRMQSPSK EKRFSP EGDQQAVDGENKLGRSMFVSDGDREAVK GGKPGEPKVGRAPHEGLGGR"
exon	complement(60793..61039)	/locus-tag="An18g01250"
intron	complement(61040..61119)	/number=1 /locus-tag="An18g01250"
exon	complement(61120..61169)	/number=1 /locus-tag="An18g01250"
gene	complement(61713..61825)	/number=2 /gene="tRNA-Leu (CAG)"
tRNA	complement(61713..61825)	/locus-tag="An18e01260" /gene="tRNA-Leu (CAG)"
gene	<61921..>62425	/locus-tag="An18e01260" /product="tRNA-Leu" /inference="profile:tRNAscan:1.4" /note="codon recognized: CUG"
mRNA	join(<61921..61955,62098..>62425)	/locus-tag="An18g01270"
CDS	join(61921..61955,62098..62425)	/locus-tag="An18g01270"
		/codon-start=1 /product="hypothetical protein" /protein-id="CAK47201.1" /db-xref="GI:134084168" /translation="MSDATRCIFITSAEWGSLRC SQQNPQFNQVDALVERPCNSTVSV TCSTAALTVD MHESRRSFSRKDQIATLRETIEYR VTVLAACDRARFPTGPEIFSTNAV RDDLTRNLGPDSINTERR"
exon	61921..61955	/locus-tag="An18g01270"
intron	61956..62097	/number=1 /locus-tag="An18g01270"
		/number=1



exon	62098..62425	/locus-tag="An18g01270"
		/number=2
gene	complement(<64435..>65520)	/locus-tag="An18g01280"
mRNA	complement(join(<64435..64754,64947..65072,65109..65228,65472..>65520))	/locus-tag="An18g01280"
CDS	complement(join(64435..64754,64947..65072,65109..65228,65472..65520))	/locus-tag="An18g01280"
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		/product="hypothetical protein"
		/protein-id="CAK47202.1"
		/db-xref="GI:134084169"
		/translation="MTTAAGWGPRLGPRPDHLNLLPGPRGAANASRKPAESESGSGFHPRPWKQNARSRAGRVSPLSLVPNFFASFCLYLVPGVDPRIWPRVRKNSIDNKLFAVLFFIATTIRCGVPLREKGMIRVITSYRATVTRREDKEASNLSKHGLLWGCLFQKEDQSKPVERGSPGGWMTESDTALDPWLRITRAGLHTEDFPYAVESWKAR"
exon	complement(64435..64754)	/locus-tag="An18g01280"
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intron	complement(64755..64946)	/locus-tag="An18g01280"
	)	
		/number=1
exon	complement(64947..65072)	/locus-tag="An18g01280"
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		/number=2
exon	complement(65109..65228)	/locus-tag="An18g01280"
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		/number=3
intron	complement(65229..65471)	/locus-tag="An18g01280"
	)	
		/number=3
exon	complement(65472..65520)	/locus-tag="An18g01280"
	)	
		/number=4
gene	<66055..>67388	/locus-tag="An18g01290"
mRNA	join(<66055..66654,66723..>67388)	/locus-tag="An18g01290"
CDS	join(66055..66654,66723..67388)	/locus-tag="An18g01290"
		/note="unnamed protein product; Title: strong similarity to hypothetical protein encoded by An13g01340 - Aspergillus niger"
		/codon-start=1
		/protein-id="CAK47203.1"
		/db-xref="GI:134084170"
		/translation="MLSLAIQSLLEADAHAAASPALQRRSSSSASTEGEAVMSPLPSLQTKGLIVISALATVSLICTLSLLTFFTYRFIFWK RHYKRYIGYNQYVVLMFNLILADF IQSLGFIISLRWIQTNSVTASDPACFLQGIWLQI

		GDPMSGLEFVLAIAAHTFMHVTLGY
		QISHRLFVSIICGLWLFVITTVIPIAAHGRYVW
		YPAVAWCWMTPKYESMRLWTHYFW
		IFASEFFTIVVLYAIMFIQLRKKIAESAILGEHNS
		ESLTRLKRVIFHMALYPVVIICLT
		LPLAAGRMASASGHSPSVLYFCFAGSFMTLCGFC
		DSLMYTLSRRSVVLEPEARIHGSS
		NKYSSRPNKSSVAHHYGN SIDGKGPTNTTIARGR
		SDSTEEMIGKDGLELAPMGVVLQH
sig-peptide	66055..66105	TTIEVTHEAAYDSASSNL SGQRERSSIIYH"
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		/inference="protein
mat-peptide	join(66106..66654,	motif:SignalP:2.0"
	66723..67385)	/locus-tag="An18g01290"
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exon	66055..66654	/locus-tag="An18g01290"
		/number=1
intron	66655..66722	/locus-tag="An18g01290"
		/number=1
exon	66723..67388	/locus-tag="An18g01290"
		/number=2
gene	<68231..>69040	/locus-tag="An18g01300"
mRNA	<68231..>69040	/locus-tag="An18g01300"
CDS	68231..69040	/locus-tag="An18g01300"
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		/inference="profile:PFAM:PF04299"
		/note="unnamed protein product;
		Remark: paiB from B. subtilis
		seems to be essential. Similarity:
		the predicted A. niger protein
		shows weak similarity to
		transcription regulator 2 of the
		pai operon of B. subtilis and
		conserved hypothetical proteins
		from several procaryotic
		organisms. Title: similarity to
		transcription regulator paiB
		-Bacillus subtilis"
		/citation=[11]
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		QNPLGVLTTAIPSSSTHPLLQSTHI
		PWVLDIPPPSTADNSNTVKLRGHIARANPQCSAI
		LDLSTTQPESILPTEVLILFTSPY
		HSYITPHFYTTTKPLTGKVAPTWNYYAAVQVYGRA
		RIYNPRSEGELGEQASMFLDTQLR
		DLTAHCEGEIMGYTTTGTSDTYTHNNPEEKSCPR
		AWTVDEAPDAYINILKKNIIGIEV
		TVTRMDGKFKMSQERGE DREGVLKGLDGMGGDV
		ARGVAGMVRECCCDTRP"
exon	68231..69040	/locus-tag="An18g01300"
		/number=1
gene	69096..69207	/gene="tRNA-Leu (CAG) "
		/locus-tag="An18e01310"
tRNA	69096..69207	/gene="tRNA-Leu (CAG) "
		/locus-tag="An18e01310"
		/product="tRNA-Leu"
		/inference="profile:tRNAscan:1.4"
		/note="codon recognized: CUG"

gene	<71863..>73356	/locus-tag="An18g01320"
mRNA	join(<71863..72033, 72097..72406, 72467..>73356)	/locus-tag="An18g01320"
CDS	join(71863..72033, 72097..72406, 72467..73356)	/locus-tag="An18g01320"

/EC-number="3.4.23.35"  
 /inference="profile:PFAM:PF00026"  
 /note="unnamed protein product;  
 Function: BAR1 of *S. cerevisiae*  
 selectively cleaves the  
 6-Leu-|-Lys-7 bond in the  
 pheromone alpha-mating factor.  
 BAR1 activity is abolished by in  
 vitro mutation of an aspartic acid  
 predicted to be in the active  
 site. Induction: secretion of BAR1  
 of *S. cerevisiae* is stimulated to  
 as much as five times the basal  
 level by exposure of cells to  
 alpha-factor. Localization: BAR1  
 of *S. cerevisiae* is secreted into  
 the periplasmic space of MATa  
 cells. Remark: BAR1 of *S.*  
*cerevisiae* is already active in  
 early compartments of the  
 secretory pathway. Bar1 protease  
 tolerates large N-terminal  
 extensions of its substrate and  
 does not require Golgi-specific  
 modifications such as outer-chain  
 glycosylation for activity.  
 Remark: the protein sequence of  
 barrier protease BAR1 of *S.*  
*cerevisiae* is covered by patent  
 WO9118988-A (AC# AAR20109). the  
 patented barrier protease is  
 useful in industrial processes  
 where leucine-lysine or  
 leucine-arginine cleavage is  
 required at low pH or high  
 temperature. barrier protease may  
 also be used in the production and  
 isolation of proteins made by  
 genetic engineering methods, e. g.  
 to cleave fusion proteins at  
 Leu-Arg bonds. Similarity: the  
 predicted *A. niger* protein shows  
 strong similarity to extracellular  
 protease precursor BAR1 of *S.*  
*cerevisiae* which belongs to the  
 subfamily A1 of aspartic-type  
 peptidases. Title: strong  
 similarity to extracellular  
 protease precursor Bar1 -  
*Saccharomyces cerevisiae*  
 extracellular/secretion proteins"  
 /citation=[2]  
 /citation=[3]  
 /citation=[8]  
 /citation=[38]

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sig-peptide	71863..71916	/locus-tag="An18g01320" /inference="protein motif:SignalP:2.0"
mat-peptide	join(71917..72033, 72097..72406, 72467..73353)	/locus-tag="An18g01320"
exon	71863..72033	/product="unnamed" /locus-tag="An18g01320" /number=1
intron	72034..72096	/locus-tag="An18g01320" /number=1
exon	72097..72406	/locus-tag="An18g01320" /number=2
intron	72407..72466	/locus-tag="An18g01320" /number=2
exon	72467..73356	/locus-tag="An18g01320" /number=3
gene	<74203..>75729	/locus-tag="An18g01330"
mRNA	join(<74203..74720, 74803..75129, 75220..75442, 75604..>75729)	/locus-tag="An18g01330"
CDS	join(74203..74720, 74803..75129, 75220..75442, 75604..75729)	/locus-tag="An18g01330"  /codon-start=1 /product="hypothetical protein" /protein-id="CAK47206.1" /db-xref="GI:134084173" /translation="MPILPRLHLFEIADQPWCPD KAIEYVQLCLTHCWNLRPLPIAKA SSADVACDVLAEFNPDISSFTFVDLGSGAGGPSS TLERLLNARLRAQHLPPAQFLITD LNPHPREWAALTKQQENISYISESVDATKCDRLV PQIRKECRMFNVAFFHFDPLAMP MLRSAIESADAFIIFELTARDFSSMLILPGLVLI AFQYTLLRFWRSPLHLLFTFVLPL APLLMVFDGFVSIMRCRTPDELHDLVRRSDAAGL ENWEFRSGKSPVMYPTTNVHWFMG VKKTAHTHTELVICVSTIKMTRWLSLMRTIAKVL QPSSSKVHSFKCGRQPGHPIGSLV SVGISGPGPRLCFYANIDHRAKMSTWTTGHSSYK

exon	74203..74720	VAWLTQPNARNPGKDPIQPGVRLA SPHPM"
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intron	74721..74802	/locus-tag="An18g01330"
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exon	74803..75129	/locus-tag="An18g01330"
		/number=2
intron	75130..75219	/locus-tag="An18g01330"
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exon	75220..75442	/locus-tag="An18g01330"
		/number=3
intron	75443..75603	/locus-tag="An18g01330"
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exon	75604..75729	/locus-tag="An18g01330"
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gene	<76028..>77800	/locus-tag="An18g01340"
mRNA	join(<76028..76190, 76240..76393, 76459..>77800)	/locus-tag="An18g01340"
CDS	join(76028..76190, 76240..76393, 76459..77800)	/locus-tag="An18g01340"
		/inference="profile:PFAM:PF00328"
		/note="unnamed protein product;
		Remark: the patent does not
		provide further information about
		the function of the protein,
		except for a claim of phytase
		activity. Similarity: the
		predicted A. niger protein shows
		strong similarity to protein
		sequence 11 from patent
		EP0684313-A/11 and several
		putative phytases. Title: strong
		similarity to sequence 11 from
		patent EP0684313-A - Unclassified
		organism"
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		/protein-id="CAK47207.1"
		/db-xref="GI:134084174"
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		SPNDPLETSEPIEGAAGRNIFHYM
		GNLSPYHVPDGFVDEYPLPKGSNITQMHHIHRH
		GSRYPPSSSEGLASWAQKIINSTAS
		GNNFTGALSFLNDWDYGLGLEILVPKGRQELYDS
		GVLNFYNYGHLYNASSPHKLVART
		TTQDRMLKSAENFLAGFFGLEWTEKANLLPIIEG
		VGYNNSLIGTYSCTRALEYMAYNA
		TTPLSTWKNIYLKARTEALRTLGTSYNWTTTDSF
		NAQDMCAYETISYGYSQFCELFTE
		EEFENFGYAFDIEFANMVGFACPAGRAQGIWVE
		EFLARVEGHLLQTTGTNANMTLDT
		NPVTFPTDQNLYLDFSHDAGIVAVLTAFGFRQFA
		ESLPATGPPLYQQFKSSKIVPFAG
		RTNIEIIKAPNQVAAIRPAGDQSDAYVDGTGETF
		YVHFLQNQRTLPLHSSFEECEYRD
		DGWCELSTFMAVQKKGLERSQFEYACFGNWTVTE
		YGTVTDGVPV"
sig-peptide	76028..76084	/locus-tag="An18g01340"
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mat-peptide	join(76085..76190, 76240..76393, 76459..77797)	motif:SignalP:2.0" /locus-tag="An18g01340"
exon	76028..76190	/product="unnamed" /locus-tag="An18g01340"
intron	76191..76239	/number=1 /locus-tag="An18g01340"
exon	76240..76393	/number=1 /locus-tag="An18g01340"
intron	76394..76458	/number=2 /locus-tag="An18g01340"
exon	76459..77800	/number=2 /locus-tag="An18g01340"
gene	complement(<77988..>79819)	/number=3 /locus-tag="An18g01350"
mRNA	complement(join(<77988.. .78215,78264..78441, 78499..79055, 79113..79172, 79229..79241, 79298..79508, 79560..79700, 79753..>79819))	/locus-tag="An18g01350"
CDS	complement(join(77988.. 78215,78264..78441, 78499..79055, 79113..79172, 79229..79241, 79298..79508, 79560..79700, 79753..79819))	/locus-tag="An18g01350"  /inference="profile:COGS:COG2141" /note="unnamed protein product; Remark: HA protein regulates homeostasis and adaptation. the C. glutamicum HA genes (I) can be used in vectors for expression in host cells and production of fine chemicals, such as, an organic acid, proteinogenic or nonproteinogenic amino acid (preferred), purine or pyrimidine base, nucleoside, nucleotide, lipid, saturated or unsaturated fatty acid, diol, carbohydrate, aromatic compound, vitamin, cofactor, polyketide or enzyme. the amino acids produced can be lysine, glutamine, glutamate,alanine, aspartate, glycine, serine, threonine, methionine,cysteine, valine, leucine, isoleucine, arginine, proline,histidine, tyrosine, phenylalanine, or tryptophan. the fine chemical production can be modulated. the presence of (I) or HA proteins encoded by then are used for diagnosing the presence or activity of Corynebacterium

diphtheriae. (I) can be used to map the *C. glutamicum* genome or can be used as markers for genetically engineered *Corynebacterium* or *Brevibacterium*. the HA proteins encoded by the (I) are used to maintain homeostasis in *C. glutamicum* or help the microorganism to adapt to different environmental conditions. Similarity: the predicted *A. niger* protein shows strong similarity to HA protein sequence SEQ ID NO:420 from patent WO200100842-A2 (AC# AAB79232), which is a monooxygenase by similarity. Title: strong similarity to HA protein sequence SEQ ID NO:420 from patent WO200100842-A2 - *Corynebacterium glutamicum*"

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 /db-xref="GI:134084175"  
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 EMCSGHQSPGLWRHPEDESHFRND  
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 RNLEPAIIISGAQWPVNEPLAVVPA  
 MAAATQNIGFGVTVTTTYEQPYHLARRLSTIDHL  
 TKGRIGWNIVTGYLDSAARNLGHT  
 QQPQHDDRYAQAE EYIKVTYKLWESSWRSDAVVL  
 DRTRGIYTDPTRVREINHSGKYFT  
 VPGPHICQSPQRTPVILQAGTSKAGKAFAAQHA  
 EAIFVAGHSPSVVAKNIAEIRETA  
 KTQFGRDPAGIKFLALLCPVLGRTEEEAQEKFRY  
 FRSLGSIDGALALFGGWTGIDLDR  
 YGDDEELRHVESNAIRSAVEGWSKATPEVEKWTK  
 ATVGQHITVGG LGATPVGTPEQVA  
 DEMERWVNEADV DGFNLAYAIKPGSFKDIIDLLI  
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 YSKEGQSGPPADHPAAKYRWHAGVEAADHPVPNY  
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		/number=1
exon	complement(78264..78441	/locus-tag="An18g01350"
	)	
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intron	complement(78442..78498	/locus-tag="An18g01350"
	)	
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exon	complement(78499..79055	/locus-tag="An18g01350"
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	)	
		/number=3
exon	complement(79113..79172	/locus-tag="An18g01350"
	)	

intron	complement(79173..79228	/number=4 /locus-tag="An18g01350"
	)	
exon	complement(79229..79241	/number=4 /locus-tag="An18g01350"
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	)	
intron	complement(79509..79559	/number=6 /locus-tag="An18g01350"
	)	
exon	complement(79560..79700	/number=6 /locus-tag="An18g01350"
	)	
intron	complement(79701..79752	/number=7 /locus-tag="An18g01350"
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exon	complement(79753..79819	/number=7 /locus-tag="An18g01350"
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gene	<80602..>83154	/number=8 /locus-tag="An18g01360"
mRNA	join(<80602..80707,	/locus-tag="An18g01360"
	80740..80815,	
	80860..80917,	
	80965..81151,	
	81201..81300,	
	81343..81426,	
	81473..81659,	
	81704..81754,	
	81802..81972,	
	82019..82337,	
	82386..82882,	
	82945..>83154)	
CDS	join(80602..80707,	/locus-tag="An18g01360"
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	80860..80917,	
	80965..81151,	
	81201..81300,	
	81343..81426,	
	81473..81659,	
	81704..81754,	
	81802..81972,	
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 import. Induction: high-level  
 expression of S. cerevisiae DUR3  
 is inducer dependent, requiring  
 functional DAL81 and DAL82 genes.  
 Regulation: expression of S.  
 cerevisiae DUR3 is regulated in a



manner similar to that of other genes in the allantoin pathway. Repression: DUR3 expression is highly sensitive to nitrogen catabolite repression and also has a partial requirement for the GLN3 product. Repression: maintenance of *S. cerevisiae* DUR3 mRNA at uninduced, nonrepressed basal levels requires the negatively acting DAL80 gene product. Similarity: *S. cerevisiae* DUR3 belongs to the major facilitator family. Title: strong similarity to urea transport protein Dur3 - *Saccharomyces cerevisiae* plasma membrane"

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Remark: mutagenesis experiments demonstrate that conserved amino acid residues, functionally critical in the human cystic fibrosis transmembrane conductance regulator (hCFTR), play a vital role in YCF1-mediated cadmium resistance. Remark: substitution of a serine to alanine residue in a potential protein kinase A phosphorylation site in a central region of YCF1, which displays sequence similarity to the central regulatory domain of hCFTR, also rendered YCF1 nonfunctional.

Remark: the YCF1 gene of *S. cerevisiae* is an MgATP-energized, uncoupler-insensitive vacuolar membrane glutathione S-conjugate transporter. Similarity: the predicted *A. niger* protein shows strong similarity to cadmium factor (YCF1) from *S. cerevisiae*, which belongs to the ATP binding cassette (ABC) protein superfamily of membrane transporters. Title: strong similarity to cadmium resistance protein Ycf1 - *Saccharomyces cerevisiae* [putative sequencing error] putative sequencing error"

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similarity to the copper
homeostasis protein CUP9 from S.
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Function: the MCT3 transporter from *Rattus norvegicus* is a proton-linked monocarboxylate transporter. it catalyzes the rapid transport across the plasma membrane of many monocarboxylates such as lactate, pyruvate, branched-chain oxo acids derived from leucine, valine and isoleucine, and the ketone bodies acetoacetate, beta-hydroxybutyrate and acetate. Similarity: the predicted *A. niger* protein shows strong similarity to the monocarboxylate transporter 3 (MCT3) of *R. norvegicus*, which belongs to the major facilitator superfamily. Title: strong similarity to monocarboxylate transporter 3 MCT3 - *Rattus norvegicus*"

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is involved in glycolysis /
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metabolism; bile acid
biosynthesis; tyrosine metabolism;
glycerolipid metabolism. Remark:
the protein sequence of alcohol
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stearothermophilus NCA1503 is
covered by patent JP04218378-A
(AC# AAR26874). Similarity: the
predicted A. niger protein shows
strong similarity to thermostable
alcohol dehydrogenase ADH-T from
B. stearothermophilus NCA1503,
which belongs to the zinc alcohol
dehydrogenase (ADH) family. Title:
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		HFLHCDQALGHEGVGVVVKHVGPSVSSVKVGDRVG FGFIRRVCGRCDNCISGCDHHCRC KRAYGQHDFDVGSFSGHTVWDADAVYPIPEGYDS AHAAPLLCAGASVWACLNNNGIRP SDRVGVMGIGGLGHLAIKLARALRYNVVALSSSE KKREEALEFGASEFYRFPNTQTPN HIKPVKHLLLCGSSDVDYASWVSHLPSKQNAIDH ANIYRSLDLVDNTNGTIYHISVTL KPTPIPLVPFGQKGIRIQGCFITSRRNLQELLEF AARFDIKPTIMTFPLTRNGLEETI EKLRAGRIRYRAVLEYQAP"
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intron	complement(101142..101213)	/locus-tag="An18g01430"
		/number=1
exon	complement(101214..101496)	/locus-tag="An18g01430"
		/number=2
gene	<101875..>104542	/locus-tag="An18g01440"
mRNA	join(<101875..101958, 102203..102219, 102259..102360, 102392..102399, 102621..103153, 103205..>104542)	/locus-tag="An18g01440"
CDS	join(101875..101958, 102203..102219, 102259..102360, 102392..102399, 102621..103153, 103205..104542)	/locus-tag="An18g01440"
		/inference="profile:COGS:COG3496" /note="unnamed protein product; Similarity: the predicted A. niger protein shows local similarity to the hypothetical protein mll8086 from M. loti. Title: strong similarity to hypothetical protein CAD70872.1 - Neurospora crassa" /codon-start=1 /protein-id="CAK47217.1" /db-xref="GI:134084184" /translation="MTAKCMVIKKAEDHTEFLG LHHVGSCKNFDNCVTKEVRGPQIL KKFLLRQWIPAQGGREQQPESLILSPVRKNLPSI SVDGILLHAALLTVNLILKLGGWP GLLKFMLRTFAISSVLAPIGLIGFLVLSFTPRN IKSLSKDKSVIGKPLLFPITLDHT RLSPIKNNFTFNVLFVGIPVGISCRFGRLLSIDA KHTDEEECTERSLLRLLQTYFSS WFSFDSARYLHRGDDTLLENKLNKFLREQNENP AKWPYAYMLSVPRFLWWERSVVTW WYLYSESKELDAVIMEINNSFDEKRNVLFKVRRT RIYTESPEKGFEQLLDCKEEHLDE DKRVFSLIPQHGKYAYKATWKKEIFSSPFKEKVG TVSSTFLDPVPSSWSGNRSLSNT TTFDPSGAPRMIALRWCKVPPIDPGKASSFQIFS ILLIWTNVNLTATPRILFQAIRLH VMNLMRMEHPDVRPGSEPRRPSKGERKDAPLKM LHSLFDLHANLQSRMLERFFREYL

		KHIVASYPGDLEVITYIPCKSVFKTTICLRSTQYS AEGQDPRRLRLEVMDPAFYSRIVN SPNAGTAMAKETKPGRSPADALSSPVIASDITQS LQLLDVTVSENRTYDKACSRISW VLCLRRWLTSSFMDSFVCKALPPRTQEEYVSCLI QLWLEKLTWDFLSPHQIYRVIRAA MLQWAICWILF"
exon	101875..101958	/locus-tag="An18g01440"
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		/number=1
exon	102203..102219	/locus-tag="An18g01440"
		/number=2
intron	102220..102258	/locus-tag="An18g01440"
		/number=2
exon	102259..102360	/locus-tag="An18g01440"
		/number=3
intron	102361..102391	/locus-tag="An18g01440"
		/number=3
exon	102392..102399	/locus-tag="An18g01440"
		/number=4
intron	102400..102620	/locus-tag="An18g01440"
		/number=4
exon	102621..103153	/locus-tag="An18g01440"
		/number=5
intron	103154..103204	/locus-tag="An18g01440"
		/number=5
exon	103205..104542	/locus-tag="An18g01440"
		/number=6
gene	<106231..>106803	/locus-tag="An18g01450"
mRNA	join(<106231..106565, 106647..>106803)	/locus-tag="An18g01450"
CDS	join(106231..106565, 106647..106803)	/locus-tag="An18g01450"

/EC-number="1.14.-.-"  
 /note="unnamed protein product;  
 Function: ordA of A. parasiticus  
 is involved in the aflatoxin  
 biosynthesis and converts  
 O-methylsterigmatocystin (OMST) to  
 aflatoxins B1 or G1 and converts  
 dihydro-O-methylsterigmatocystin  
 (DHOMST) to aflatoxins B2 or G2.  
 Remark: aflatoxins comprise a  
 group of polyketide-derived  
 carcinogenic mycotoxins. Remark:  
 it is assumed that the ORF is  
 N-terminally shorter and has  
 another start codon 5' to the  
 predicted one ; the ORF is around  
 400 amino acids shorter than most  
 of the homologues cytochrome p450  
 proteins. Remark: ordA of A.  
 parasiticus is also called  
 cytochrome p450 64, cyp64 or omst  
 oxidoreductase. Similarity: the  
 ORF shows similarity to several  
 cytochrome P450 related proteins  
 from different species. Title:  
 strong similarity to  
 O-methylsterigmatocystin  
 oxidoreductase ordA - Aspergillus

		parasiticus"
		/citation=[43]
		/codon-start=1
		/protein-id="CAK47218.1"
		/db-xref="GI:134084185"
		/translation="MTFNPERFLTITESYQAEHDP HNLAFGFGRRICPGRGFADSTIFL TVVRSLLQAFRIAKISEDGREIEPIVEYLPGVISH PKPFAISITPRSKEHESFIRSIEI EHPWEKGDVLSILSVNVLVVVASKLRVFTILTSL YRLPLIGNCKPPNLLLGRMGLIRF SLH"
exon	106231..106565	/locus-tag="An18g01450"
		/number=1
intron	106566..106646	/locus-tag="An18g01450"
		/number=1
exon	106647..106803	/locus-tag="An18g01450"
		/number=2
gene	<107279..>108340	/locus-tag="An18g01460"
mRNA	join(<107279..107327, 107380..107740, 107795..107907, 107966..107988, 108045..108097, 108151..>108340)	/locus-tag="An18g01460"
CDS	join(107279..107327, 107380..107740, 107795..107907, 107966..107988, 108045..108097, 108151..108340)	/locus-tag="An18g01460"

/EC-number="1.-.-.-"  
 /inference="profile:COGS:COG1028"  
 /inference="profile:PFAM:PF00106"  
 /note="unnamed protein product;  
 Catalytic activity: cyclohexanol  
 dehydrogenases convert  
 cyclohexanol + NAD(+) <=>  
 cyclohexanone + NADH. Function:  
 chnA of A. sp. is an alcohol  
 dehydrogenases proposed to  
 catalyze the conversion of  
 cyclohexanol to cyclohexanone (EC  
 1. 1. 1. 245). Phenotype:  
 cyclohexanol was detected as the  
 major intermediate accumulated in  
 the chnA mutant of A. sp. Remark:  
 chnA of A. sp. is encoded in the  
 gene cluster for cyclohexanol  
 oxidation. Similarity: the ORF  
 shows similarity to several  
 dehydrogenases from different  
 species and with various  
 specificities. Title: strong  
 similarity to cyclohexanol  
 dehydrogenase chnA - Acinetobacter  
 sp"  
 /citation=[57]  
 /codon-start=1  
 /protein-id="CAK47219.1"  
 /db-xref="GI:134084186"  
 /translation="MAHLLQGTAFTGAGSGIGA  
 GVARTFIQNGISKLLALVDINLSIL

		QKVSESLKQTFPNVELLTSAVDVTNEVHVDNAVQ KAATTFGRVDIGVNSAGVGDPEG TDRLSLKDQRTVHINQTVWLSQRALIQQLTQ KSRGTRHGRGVIVNVCSLGITAS ATGIFFPAYTSSKHGVMGLTKMDAKYYAPSGIRI NAVCPGFVDTPMVSKAVDSGVFVK EVESAPVGRIGDVEEITDSILFLASPMSSFIYGA GLVVDGGYGL"
sig-peptide	join(107279..107327, 107380..107387)	/locus-tag="An18g01460"
		/inference="protein motif:SignalP:2.0"
mat-peptide	join(107388..107740, 107795..107907, 107966..107988, 108045..108097, 108151..108337)	/locus-tag="An18g01460"
		/product="unnamed"
exon	107279..107327	/locus-tag="An18g01460"
		/number=1
intron	107328..107379	/locus-tag="An18g01460"
		/number=1
exon	107380..107740	/locus-tag="An18g01460"
		/number=2
intron	107741..107794	/locus-tag="An18g01460"
		/number=2
exon	107795..107907	/locus-tag="An18g01460"
		/number=3
intron	107908..107965	/locus-tag="An18g01460"
		/number=3
exon	107966..107988	/locus-tag="An18g01460"
		/number=4
intron	107989..108044	/locus-tag="An18g01460"
		/number=4
exon	108045..108097	/locus-tag="An18g01460"
		/number=5
intron	108098..108150	/locus-tag="An18g01460"
		/number=5
exon	108151..108340	/locus-tag="An18g01460"
		/number=6
gene	<108826..>111209	/locus-tag="An18g01470"
mRNA	join(<108826..108944, 109020..109023, 109089..109305, 109377..109778, 109841..109905, 110160..110181, 110244..110293, 110355..110492, 110524..110752, 110866..110960, 111135..>111209)	/locus-tag="An18g01470"
CDS	join(108826..108944, 109020..109023, 109089..109305, 109377..109778, 109841..109905, 110160..110181, 110244..110293, 110355..110492, 110524..110752, 110866..110960,	/locus-tag="An18g01470"

111135..111209)

/EC-number="1.14.-.-"  
/inference="profile:COGS:COG0493"  
/note="unnamed protein product;  
Remark: aflatoxins are  
polyketide-derived secondary  
metabolites. Remark: moxY of A.  
parasiticus is expressed  
concurrently with genes involved  
in aflatoxin biosynthesis and it  
lies on one end of the cluster of  
this genes. Therefore moxY of A.  
parasiticus is presumably also  
involved in aflatoxin  
biosynthesis. Similarity: the ORF  
shows similarity to monooxygenases  
from several species and with  
different functions. Title: strong  
similarity to monooxygenase moxY  
-Aspergillus parasiticus"  
/citation=[55]  
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/protein-id="CAK47220.1"  
/db-xref="GI:134084187"  
/translation="MANEQTCSPSINLNTHENMC  
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TQIELCTVLFASFNMISASTTDTFTQVIIIGAGM  
SGLAMACQLKKQLCCEDFVIYDRA  
PSFGGTWYFNKCCGVDIPAAFYSFSFALYPQFTC  
FFPKQEEILQYIHGVADEFSVALK  
LVGHTEWEGADWQDSEQCWEVRLREIPSGRKFT  
RCRILISAVGGLTNPKHVMLQGIE  
RFQGNIVHTALWDQETAVAGKNVIVIGNGASATQ  
FIPAIADDAASINQFIRHVRKCAP  
EEQYWSLLTPEYSIGCKRRVFDNDGYLKCLHRPN  
VDITNDPVVAVEEQSITTQSGKRF  
PADLIADVLDYGRCLRLGSLSRSTMSTGEVVMG  
VRDKNIGTVSAAYKHLRRWPWRNF  
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RFNTKLKSALRKTFTNMCRSLPA  
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exon	108826..108944
intron	108945..109019
exon	109020..109023
intron	109024..109088
exon	109089..109305
intron	109306..109376
exon	109377..109778
intron	109779..109840
exon	109841..109905
intron	109906..110159
exon	110160..110181

intron	110182..110243	/number=6 /locus-tag="An18g01470"
exon	110244..110293	/number=6 /locus-tag="An18g01470"
intron	110294..110354	/number=7 /locus-tag="An18g01470"
exon	110355..110492	/number=7 /locus-tag="An18g01470"
intron	110493..110523	/number=8 /locus-tag="An18g01470"
exon	110524..110752	/number=8 /locus-tag="An18g01470"
intron	110753..110865	/number=9 /locus-tag="An18g01470"
exon	110866..110960	/number=9 /locus-tag="An18g01470"
intron	110961..111134	/number=10 /locus-tag="An18g01470"
exon	111135..111209	/number=10 /locus-tag="An18g01470"
gene	<111907..>113460	/number=11 /locus-tag="An18g01480"
mRNA	<111907..>113460	/locus-tag="An18g01480"
CDS	111907..113460	/locus-tag="An18g01480"

/inference="profile:COGS:COG2124"  
 /inference="profile:PFAM:PF00067"  
 /inference="similar to AA  
 sequence:UniProtKB:AB013443.1"  
 /note="unnamed protein product;  
 Function: eln2 of C. cinereus  
 encodes a novel type of microsomal  
 cytochrome P450 enzyme, with is  
 involved in mushroom  
 morphogenesis. Phenotype: a  
 dominant mutation of the  
 elongationless2 (eln2) gene of the  
 mushroom C. cinereus affects  
 pattern formation in the  
 development of fruit body  
 primordia, causing dumpy primordia  
 which culminate in mature fruit  
 bodies with short stipes.  
 Similarity: the ORF shows  
 similarity to several cytochrome  
 p450 related proteins from  
 different species, which have  
 different cellular functions.  
 Title: strong similarity to  
 cytochrome p450 related protein  
 eln2 - Coprinus cinereus"  
 /citation=[54]  
 /codon-start=1  
 /protein-id="CAK47221.1"  
 /db-xref="GI:134084188"  
 /translation="MPTILLTLLALLTLRLLYEY  
 KRDRNLPPGPRRLPLIGNLHQAPQ  
 TLPWRVFDQWSKTYGPIMSAQFGRQTLILITSPT  
 IARDLLDKRGSIIYADRPDLVMANN  
 ITKGLHMLIRQYDDWLRLHQRLDAPLLSPRASNT  
 YHPIQDLESKQLMFDLLRSNDFDA  
 HFERYSGSLMFALAYGFRLSPKGQELRDMRTIQ  
 GNFTYAARVGTWIVDAIPVLNLYLP



		AVVAPWKRLAEKLFKLEASVHTRHLEKGLNSEPW NWSKEFAASKHAEGMPRLDLAYNL GILVDAGFETTWTVMKIFVLAMRSDPRFVAVARK ELDEVVGEDRMPTFEDQEKLVIYIQ AVVDETLRWRSMAFGGIPHAARKEDTYMGYRIPK GATVIPLFWSMCLTDEPWDDPLEF RPERWFEATEKEEGFRNFFGYGRRICTGRHIAR NSLFLLMARILWAFDIQAPLGDDG KVPVPVDDMAFDSAFVSTPEPFALFVPRSEKTKE IVEREWNEMEKDMAVLMGQVRDSQ RALGLDVRA"
sig-peptide	111907..111957	/locus-tag="An18g01480"
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		motif:SignalP:2.0"
mat-peptide	111958..113457	/locus-tag="An18g01480"
		/product="unnamed"
exon	111907..113460	/locus-tag="An18g01480"
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mRNA	complement(join(<113565	/locus-tag="An18g01490"
	..114153,	
	114210..>114733))	
CDS	complement(join(113565.	/locus-tag="An18g01490"
	.114153,	
	114210..114733))	
		/inference="profile:COGS:COG0598"
		/inference="profile:PFAM:PF01544"
		/inference="similar to AA
		sequence:UniProtKB:SC41293.1"
		/note="unnamed protein product;
		Function: alr2 of S. cerevisiae is
		an uptake transporter for
		inorganic cations, e. g.
		magnesium, which presence seems to
		be important for resistance to the
		toxic effect of aluminum. Remark:
		alr2 of S. cerevisiae is also
		called YFL050C. Similarity: the
		predicted ORF is 395 amino acids
		shorter at the N-terminus and 57
		amino acids shorter at its
		C-terminal end than alr2 of S.
		cerevisiae (nearly the same is
		true for alr1 of S. cerevisiae).
		Title: strong similarity to ion
		transporter Alr2 -Saccharomyces
		cerevisiae plasma membrane"
		/citation=[40]
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		/db-xref="GI:134084189"
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		RLNFFTSQNLNTSIEASSIEDLCSV
		YRPFELLLETGAHSGLWLDITAPSEEDIEALAR
		FFNLHPLTTEDIKTRETRKIELF
		GQYYFLSLRPPRRLETDGTGVRIVSHNLYAVVFRG
		GVLSFSFDPSLHTSHVRQRIKEHS
		SHLLLTSDWICYALIDDIVDGFAPFISRVENG
		TVEDSVSITRPDDMGLALQRIFKL
		RKEVMNIRQPLHDKIDVIRSFARHCDISDTSSSQ
		VALYLSDICDHVVTMIANLEQAEQ

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                                MLSRLQSKYLTQVHFDSGRMRNGIASALSKLTVL
                                ASILVPMQFITGLFGMNVVRPGKT
                                HDGDNSLTWWFSILGFILGLTVIFAWVAKRIGLL
                                DR"
exon      complement(113565..1141 /locus-tag="An18g01490"
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intron    complement(114154..1142 /locus-tag="An18g01490"
09)
                                /number=1
exon      complement(114210..1147 /locus-tag="An18g01490"
33)
                                /number=2
gene      complement(<115549..>11 /locus-tag="An18g01500"
6444)
mRNA      complement(join(<115549 /locus-tag="An18g01500"
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116080..>116444))
CDS       complement(join(115549. /locus-tag="An18g01500"
.115734,115791..116016,
116080..116444))
                                /note="unnamed protein product;
                                Title: strong similarity to
                                hypothetical protein encoded by
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                                ELTPDNIMWDTRALELFLFDHFHD
                                CRGFAKCEYPQNPPYGVYREIGDVKFGQLLECGK
                                FNWYAVSVTDYPGENLPHIKAIVE
                                NDAIGDDKLLRGEIMTITDIMKARLSNTLRPHI
                                VAPMLVLVSLMGPRHARVLEADFDG
                                VMLNIRASGLYDFTRKNTDAVQLLTRYWLGACG
                                QTTKKS"
exon      complement(115549..1157 /locus-tag="An18g01500"
34)
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intron    complement(115735..1157 /locus-tag="An18g01500"
90)
                                /number=1
exon      complement(115791..1160 /locus-tag="An18g01500"
16)
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intron    complement(116017..1160 /locus-tag="An18g01500"
79)
                                /number=2
exon      complement(116080..1164 /locus-tag="An18g01500"
44)
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gene      complement(<117672..>11 /locus-tag="An18g01510"
8234)
mRNA      complement(join(<117672 /locus-tag="An18g01510"
..117782,
117885..118021,
118123..>118234))
CDS       complement(join(117672. /locus-tag="An18g01510"
.117782,117885..118021,

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118123..118234))
/feature=1
/note="unnamed protein product;
Remark: the ORF is questionable
due to its suboptimal intron-exon
structure and short lenght Title:
questionable ORF"
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/protein-id="CAK47224.1"
/db-xref="GI:134084191"
/translation="MREQDNDRFMLPITLPNHCH
SGSDVGLPPFACQSLGWQTNVAVLG
PVYGKFAESIAIILLCIFGQWDEDLVTRGNIIIS
GVDGETLTKVLLPVLTMKRTWLKG
YHLLIGGVAVCLCVCFV"
exon complement(117672..1177 /locus-tag="An18g01510"
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intron complement(117783..1178 /locus-tag="An18g01510"
84)
/number=1
exon complement(117885..1180 /locus-tag="An18g01510"
21)
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intron complement(118022..1181 /locus-tag="An18g01510"
22)
/number=2
exon complement(118123..1182 /locus-tag="An18g01510"
34)
/number=3
gene <119176..>120297 /locus-tag="An18g01520"
mRNA <119176..>120297 /locus-tag="An18g01520"
CDS 119176..120297 /locus-tag="An18g01520"
/EC-number="1.-.-.-"
/inference="profile:COGS:COG0673"
/inference="profile:PFAM:PF01408"
/inference="similar to AA
sequence:UniProtKB:ENQUTCH.2"
/note="unnamed protein product;
Function: due to the presence of a
putative 'zinc cluster' motif and
its low (16%) but significant
similarity with the DNA-directed
DNA polymerase of hepatitis B
virus,it was assumed that qutH of
A. nidulans is a DNA-binding
protein, which is possibly
involved in the regulation of
genes essential for the
utilisation of protocatechuic
acid. Function: due to the
similarity of the ORF to
oxidoreductases, it is here
assumed that the ORF is encoding a
protein with oxidoreductase
activity. Similarity: the ORF
shows similarity to several
oxidoreductases from different
species. Title: strong similarity
to quinic-acid utilisation gene
qutH - Aspergillus nidulans"
/citation=[10]
/codon-start=1

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		<pre> /protein-id="CAK47225.1" /db-xref="GI:134084192" /translation="MLNVIIVGAGLIGPRHAQSV ITNPSTNLLALVDPSPSASSVAKT LNTLYFPSLSALLSSVPNIPHPDAAIICTPNHTH VPVALELISHNIHILLEKPISDTI TTALPLLQAQQKYPDVKILIGHHRRFNPYITKTK EILESGSLGPPIIALSGLWTLYKPA SYFTGATEWRRDKAKGGVLSINLIHDVDLLHYLF GPITRVYAEKTL PQRG GPDGNENH TAE EGAAITFRFASGVVGT FVVS D CAPSPWNFEA GTGENPIIPKVGGVGGGLYRVLGS RGSLSVPDLKRWSYDGVEGEKGWNQRLQVEEFEV DEGV PFDLQLEHFVRVLERGETPR CDAVEGLRALVVVDAVKRAMETEEVVKVESVEEI LARNE" </pre>
sig-peptide	119176..119226	<pre> /locus-tag="An18g01520" /inference="protein motif:SignalP:2.0" </pre>
mat-peptide	119227..120294	<pre> /locus-tag="An18g01520" /product="unnamed" </pre>
exon	119176..120297	<pre> /locus-tag="An18g01520" /number=1 </pre>
gene	complement(<120373..>121787)	<pre> /locus-tag="An18g01530" </pre>
mRNA	complement(join(<120373..120856,120912..121419,121479..121515,121584..>121787))	<pre> /locus-tag="An18g01530" </pre>
CDS	complement(join(120373..120856,120912..121419,121479..121515,121584..121787))	<pre> /locus-tag="An18g01530" </pre>

/note="unnamed protein product;  
 Function: pth11 of M. grisea is  
 involved in host surface  
 recognition for the initiation of  
 appressorium formation, which is  
 important in plant infection.  
 Phenotype: M. grisea pth11 mutants  
 are nonpathogenic due to a defect  
 in appressorium differentiation.  
 Remark: on the same contig another  
 ORF shows similarity to pth11 of  
 M. grisea, see 130cg. Similarity:  
 the ORF is 85 amino acids shorter  
 at its N-terminus and 155 amino  
 acids shorter at the C-terminal  
 end than pth11 of M. grisea.  
 Title: strong similarity to  
 integral membrane protein PTH11 -  
 Magnaporthe grisea"  
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		/number=4
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/inference="similar to AA  
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Function: TRI101 of F. sporotrichioides conferred significant increased tolerance to the mycotoxin DAS (trichothecene 4,15-diacetoxyscirpenol), which is harmful for vertebrates. Function: TRI101 of F. sporotrichioides converts isotrichodermol to isotrichodermin and is required for the modification of T-2 toxin, which inhibits protein synthesis in eukaryotes. Phenotype: TRI101 mutants of F. sporotrichioides were altered in their abilities to synthesize T-2 toxin and accumulated isotrichodermol and small amounts of 3,15-didecalonectrin and 3-decalonectrin, trichothecenes. Title: strong similarity to trichothecene 3-O-acetyltransferase TRI101 - Fusarium sporotrichioides"

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CDS	complement(join(123984..124060,124183..125132, 125181..125432, 125485..125732, 125913..127145))	/locus-tag="An18g01550"  /note="unnamed protein product; Title: similarity to hypothetical protein AAM43672.1 - Dictyostelium discoideum" /codon-start=1 /protein-id="CAK47228.1" /db-xref="GI:134084195" /translation="MRPIVADVNDNDGHIELKRG LCAVLETIESSGSFLTQDLGLGLA IPGLNIAGLGNIRLPISADDAKAITQCCDRSPYG KGSETLVDESVRKTWQLDPGQFSL QNPLWQQQMDDVVDVAVTGLGLTAQSDEVQAELY KLLIYEEGAFFLPHQDTEKADGMF ATLVVCLPSKHEGGTLVASHRGWKIAWSTASSSE FSFSWAAWYADVIHEVRPVTSGYR VALVYNLIHRPLVGLGISGVQTDKLTLLLESWVS DCSGNGQSDHSAWDHHINGDCPPA LVYVLEHQYTVVELSFDRLKGVQVRFGEQKAC QGLDFDLYLANIEKTRMGGVDGRY GNSYWKAHNALEDVLGGNQKFLSVVDASGSEVGK RLPFHGKLLIQEDFFSNRLPDDEK YQGFTGNEAAKATRVYRATLFSEQPDNALTKRNL VRACQTILKKHSSSEMRAKVMQI AIDVDDVILFCQTLVSLEGTMSSEITQTAKVLA

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		/number=5
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mRNA	join(<127862..127973, 128149..128238, 128310..128432, 128566..128684, 128777..128854, 128935..129026, 129125..>129230)	/locus-tag="An18g01560"
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		/note="unnamed protein product; Remark: the ORF is questionable due to its suboptimal intron-exon structure. Title: questionable ORF"

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/note="unnamed protein product;  
Function: pth11 of M. grisea pth11  
is involved in host surface  
recognition for the initiation of  
appressorium formation, which is  
important in plant infection.  
Phenotype: M. grisea pth11 mutants  
are nonpathogenic due to a defect  
in appressorium differentiation.



Remark: on the same contig another ORF shows strong similarity to pth11 of *M. grisea*, see 160wg. Similarity: the ORF is 92 amino acids shorter at the N-terminal end and 165 amino acid its C-terminus than pth11 of *M. grisea*. Title: similarity to integral membrane protein PTH11 - Magnaporthe grisea"  
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intron	130131..130175	/locus-tag="An18g01570" /number=4
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CDS	complement(join(131646..132295, 132363..132375))	/locus-tag="An18g01580"  /EC-number="4.2.1.1" /inference="profile:COGS:COG0288" /inference="profile:PFAM:PF00484" /inference="similar to AA sequence:UniProtKB:AB040135.1" /note="unnamed protein product; Catalytic activity: pcal of P. purpureum converts H(2)CO(3) <=> CO(2) + H(2)O with the usage of zinc as cofactor. Function: carbonic anhydrases catalyze the reversible hydration of carbon dioxide. Remark: an alternate name for pcal of P. purpureum is gtpcal. Similarity: the ORF shows similarity to several carbonic anhydrases from different species and with various cellular functions. Title: strong similarity to carbonic anhydrase pcal - Porphyridium purpureum" /citation=[32] /citation=[62] /codon-start=1 /protein-id="CAK47231.1" /db-xref="GI:134084198" /translation="MAVTDLHSQQPEKPQDPYTK ALTLNHLWAQKTTLQNPSLFPTLA RAQHPQILWIGCSDSRCPETTLDDLKPGDVVFVHR NIANVVNAADVNC AAVVEYAVLHL KVKHVVVCGHTCCGGVGAVLAAPKGERDGEDGEK SVLDAWLSSLKRVDRYASELEGI HGEYERGVRLVELNVLEGVRVLMAMGVVREAVEK GEVEVHGAVYNVGC GVVRELELEV KL"
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a component of the multi
subunitcomplex, which binds to RNA
polymerase II and is essential for
efficient establishment of the
transcription initiation
apparatus. Phenotype: the S.
cerevisiae srb4 the null mutant is
inviabile and srb4 mutants display
global defects in mRNA synthesis.
Remark: an alternate name for srb4
of S. cerevisiae is YER022w.
Title: strong similarity to RNA
polymerase II suppressor protein
Srb4 - Saccharomyces cerevisiae
nucleus"
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		IKELDRATSPKKKSAPTRLIKHGDKGPECLYSKHL QIGPKYRMELIKLMLENERILGEK AIQDAFDEAFFKTNFWTLWATTFALQPWHSLEVEF RRCLCKHLAEIERLNDVKALDRTK YTIYESVIMPIESYLKSQGVDFHFNAKVNTNLQIN PKEAQTTVSGIIIKDNGEQKTIEV RPEDLVMVTLGSTTSATERGSNDKAPAAPPQHSHK EFLDDDWALWIDLMQASTDYGNPF NFHNNVDQSTLESFTVTLRDSDFMERYEKLTTNNK PGTGALLSFSDSNWGLSISVPRQP VCSDQPSSVDVFWGYGLHPEKTGNFVHKPMCHCS GKEILTEVLSQLGMPVDDMLANSI TNPVLMPMATAPLMRRHDYRPEVIPPPQSRNLAL VGQYVEIQDDTTLSMEYSVRGAQM AVFSAMKLNKHPKIERHLLLSVFDLLGGA"
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		/number=1
exon	complement(142735..143279)	/locus-tag="An18g01620"
		/number=2
gene	<144032..>145578	/locus-tag="An18g01630"
mRNA	join(<144032..144169, 144230..145373, 145427..>145578)	/locus-tag="An18g01630"
CDS	join(144032..144169, 144230..145373, 145427..145578)	/locus-tag="An18g01630"
		/EC-number="1.5.3.-" /inference="profile:COGS:COG0277" /inference="profile:PFAM:PF01565" /note="unnamed protein product; Catalytic activity: HDNO of A. oxidans catalyses (D)-6-hydroxynicotine + H(2)O + O(2) = 1-(6-hydroxypyrid-3-yl)-4-(methyla mino)butan-1-one + H(2)O(2). Induction: HDNO of A. oxidans requires FAD in the enzymatic assay for maximal enzyme activity. Similarity: the ORF shows similarity to several FAD-dependent oxygenases from different species and with various specificity. Title: strong similarity to 6-hydroxy-D-nicotine oxidase 6-HDNO - Arthrobacter oxidans" /citation=[4] /codon-start=1 /protein-id="CAK47236.1" /db-xref="GI:134084203" /translation="MPFLSFARALELRRQLEGTR AEVVCIGSDDYATSIRRWSDTCEK EAGAVVRVTSTSEVAEVVRFCKNHIDFVVEAGG HSTTGASSSHGGVVISMARMCKVL TDPASETVCVQGGANWDMVNHSTAPYGLAVVGAT ASHSGVGGSALGGFGWLTGQHGL

		IADQLLSVKMVLADGSIVEASDEDNQDLFWAVRG AGQAFGVATEFVFRAHKVRDRFFG GLVYYDVKLPMLVSFANEFDKRQDPKSGFFFG AAPREIGHMVVLAVLFYDGSAYDG EAFFEPILNPNPLINRAAMKSYIEMNSIANVDPV PEGRKSIGGANIMPPLETSLLQNL YSQFKEAMNTYPRMEDSALVFELLPYTKAVQVPI KETACANRGPYYNVGLILCWHDS LDAKMHALQRSIIISKILEAQRDITDDHAVVYPNL AGHDVSAEKLFGANLPRQLKLKKK YDPHNVFRKWHDLAPARSHVEQTDKP"
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intron	144170..144229	/locus-tag="An18g01630" /number=1
exon	144230..145373	/locus-tag="An18g01630" /number=2
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exon	145427..145578	/locus-tag="An18g01630" /number=3
gene	<146433..>148685	/locus-tag="An18g01640"
mRNA	join(<146433..146489, 146546..146952, 146998..147273, 147331..147795, 147845..147954, 148006..>148685)	/locus-tag="An18g01640"
CDS	join(146433..146489, 146546..146952, 146998..147273, 147331..147795, 147845..147954, 148006..148685)	/locus-tag="An18g01640"

/EC-number="2.4.1.-"  
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 /inference="similar to AA  
 sequence:PIR:T00130"  
 /note="unnamed protein product;  
 Function: TSase of G. frondosa  
 catalyzes the trehalose synthesis  
 from alpha-D-glucose 1-phosphate  
 and D-glucose. Similarity: the ORF  
 shows similarity to a  
 clock-controlled gene (ccgs) of N.  
 crassa with unknown function.  
 Title: strong similarity to  
 trehalose synthase TSase - Grifola  
 frondosa"  
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 EKNTEKIIISAALHQSLVYRCPSLC  
 SRLWSELDIVPLVLEHKDRERRHDDQGELATFAG  
 WNKKELDERADSMVRKCIRSF  
 GIG  
 HVLHNNHINFDGSVDVDRGYHVHLANAKDYEKTVD  
 PATWSMAQCFAQDLREREVKVAFF"



		SMTCCQGKPDVPTRHLSRFTKSLGVRIKWFEVPKP RPGMIPLIRKMQDTLEGQGDPLSD ITINDELLILDFAYANARRYWLCENGPLRPRAEG GVDVVIIDSAPLLTLAILSKQQDP ERPVIFESSLQPQGVSLSGTSSPQSRWDFIRTR LTHVDLVVSLLPKELAPRIMPEEN VGYMSFSVDQLDGQNKPLTDWDVGFYGREFSSLC RTLQMSIIRYPEEQYILHLSQFRP GDGTLCLLSYQKFCDAYTKEHPGRQVPKLLICH RGPFRTPESTVFYDAAMSQIDSSE TLSTSVCIIPIGAVDQMWNALLTNARALVQLSTL HGVPEMLLAAIQKGPVIAVREAE LFPFVHESENAILVDKGDEEGIARCFSRIFSVD VRQGECDAGFRKLSDSNTTVGNAV CWLYLASKMSRGDKFEPRGADIYKLAREEAGYNE CDWHAV"
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exon	146546..146952	/locus-tag="An18g01640"
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intron	147274..147330	/locus-tag="An18g01640"
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exon	147331..147795	/locus-tag="An18g01640"
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intron	147796..147844	/locus-tag="An18g01640"
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intron	147955..148005	/locus-tag="An18g01640"
		/number=5
exon	148006..148685	/locus-tag="An18g01640"
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gene	complement(149158..149230)	/gene="tRNA-Lys (CTT)"
		/locus-tag="An18e01650"
tRNA	complement(149158..149230)	/gene="tRNA-Lys (CTT)"
		/locus-tag="An18e01650"
		/product="tRNA-Lys"
		/inference="profile:tRNAscan:1.4"
		/note="codon recognized: AAG"
gene	<149921..>150603	/locus-tag="An18g01660"
mRNA	join(<149921..149936, 150144..150502, 150577..>150603)	/locus-tag="An18g01660"
CDS	join(149921..149936, 150144..150502, 150577..150603)	/locus-tag="An18g01660"
		/note="unnamed protein product; Remark: the ORF is questionable due to its suboptimal intron-exon structure. Similarity: the ORF overlaps with the 5' region of the A. niger pfkA gene. Title: questionable ORF"
		/codon-start=1

		/protein-id="CAK47238.1"
		/db-xref="GI:134084205"
		/translation="MKETESGDIRCFQDCKRKWA EEDIPCQHPSRICPLQRAARSPGR SAFDEHLALSPADQLSPQWWAVYSVQSTFPSNER GYLYSGAVTAGVSDVLVAHTRFFS PAPALLFSPTLQTQVISAFPPQALLLIPNNC"
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intron	149937..150143	/locus-tag="An18g01660"
		/number=1
exon	150144..150502	/locus-tag="An18g01660"
		/number=2
intron	150503..150576	/locus-tag="An18g01660"
		/number=2
exon	150577..150603	/locus-tag="An18g01660"
		/number=3
gene	<150631..>153085	/gene="pfkA"
mRNA	join(<150631..151371, 151428..151889, 151937..>153085)	/locus-tag="An18g01670"
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CDS	join(150631..151371, 151428..151889, 151937..153085)	/locus-tag="An18g01670"
		/gene="pfkA"
		/locus-tag="An18g01670"
		/EC-number="2.7.1.11"
		/inference="profile:COGS:COG0205"
		/inference="profile:PFAM:PF00365"
		/inference="similar to AA sequence:SWISSPROT:K6PF.ASPNG"
		/note="Catalytic activity: pfkA of A. niger is catalysing ATP + D-fructose 6-phosphate <=> ADP + D-fructose 1,6-bisphosphate. Function: pfkA of A. niger is active in a key control step of glycolysis. Gene-ID: pfkA Similarity: the ORF overlaps with the sequence of entry EMBL:ANPFKA (A. niger pfkA gene) cytoplasm"
		/citation=[1]
		/citation=[5]
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		/db-xref="InterPro:IPR000023"
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		GKRRITIVIVAEGAQDRHLNKISSS KIKDILTERLNLDTRVTVLGHTQRGGAACAYDRW LSTLQGVEAVRAVLDMKPEAPSPV ITIRENKILRMPLMDAVQHTKTVTKHIQNKEFAE AMALRDSEFKEYHFSYINTSTPDH PKLLLLPENKRMIRIGIIHVGAPAGGMNQATRAAVA YCLTRGHTPLAIHNGFPGLCRHYD DTPICSVREVAWQESDAWVNEGGS DIGTNRGLPG DDLATTAKSFKKFGFDALFVVGGF EAFTAVSQLRQAREKYPEFKIPMTVLPATISNNV PGTEYSLGSDTCLNTLIDFCDAIR QSASSRRRVFVIETQGGKSGYIATTAGLSVGAV AVYIPEEGIDIKMLARDIDFLRDN FARDKGANRAGKII LRNECASSTYTTQVVADMIK EEAKGRFESRAAVPGHFQQGGKPS PMDRIRALRMATKMLHLESYAGKSAD EIAADEL SASVIGIKGSQVLFSPMGGGETGLE ATETDWARRRPKTEFWLELQDTVNILSGRASVNN ATWSCYENA"
exon	150631..151371	/gene="pfkA" /locus-tag="An18g01670" /number=1
intron	151372..151427	/gene="pfkA" /locus-tag="An18g01670" /number=1
exon	151428..151889	/gene="pfkA" /locus-tag="An18g01670" /number=2
intron	151890..151936	/gene="pfkA" /locus-tag="An18g01670" /number=2
exon	151937..153085	/gene="pfkA" /locus-tag="An18g01670" /number=3
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mRNA	complement(join(<153410..153429, 153509..>154508))	/locus-tag="An18g01680"
CDS	complement(join(153410..153429, 153509..154508))	/locus-tag="An18g01680"

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 /inference="profile:PFAM:PF00070"  
 /inference="similar to AA  
 sequence:UniProtKB:AF281147.1"  
 /note="unnamed protein product;  
 Catalytic activity: NADH  
 dehydrogenases catalyse NADH +  
 acceptor <=> NAD(+) + reduced  
 acceptor. Function: ndh of P.  
 fluorescens is involved in  
 colonization of this bacterium.  
 Phenotype: in an oxygen-poor  
 medium mutant PCL1201 of P.  
 fluorescens, which carries a  
 mutation in the ndh gene showed a  
 decreased growth rate. Remark: the  
 sequence of the database entry  
 EMBL:ANPFKA (A. niger pfkA gene)  
 overlaps with the ORF due a

probably wrong number of 4658 bp  
for the coding sequence of the A.  
niger protein, which is encoded  
3'. Similarity: the ORF is 112  
amino acids shorter at its  
C-terminal end than ndh of P.  
fluorescens. Title: similarity to  
NADH dehydrogenase II ndh  
-Pseudomonas fluorescens  
localisation:mitochondrion"  
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LLQVEESTTNNTNKALREIKYDYLVIASGSTPSA  
SSSSPLFPGETETENKADADRKEVI  
YPFKLSPTSTSTITETIQSAQHTISTSKKITIIG  
AGPIGVELAGELADLTSSASSKEK  
KDITLISSTPRILPVLKESASGTATSLTSGKVR  
VLTNTKVISVSASKEGGGGYELKF  
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		/number=1
exon	complement(153509..154508)	/locus-tag="An18g01680"
		/number=2
gene	complement(<154789..>156395)	/locus-tag="An18g01690"
mRNA	complement(join(<154789..154869, 154921..155060, 155120..155914, 155981..156128, 156179..156193, 156245..156318, 156371..>156395))	/locus-tag="An18g01690"
CDS	complement(join(154789..154869,154921..155060, 155120..155914, 155981..156128, 156179..156193, 156245..156318, 156371..156395))	/locus-tag="An18g01690"
		/inference="similar to AA sequence:PIR:S67043"

		/note="unnamed protein product; Title: strong similarity to hypothetical protein YOR155c - Saccharomyces cerevisiae" /codon-start=1 /protein-id="CAK47241.1" /db-xref="GI:134084208" /translation="MTTRYRVEYALKVGSHLCCQ SMLTPAVSPSRPIIEWIKGLLAVP FVLHSQPTAVYQEHSENLIAVAADTHQRYAEIFR DVEMLIRDHITHQQDDAPGKSKLK LLVPTVGTFFTPLYLVDAFRRQDAQRFISRRRFV APSFNDIRLILNSAQLIGLARTTG VDLVTFDGDVTLYDDGACLTDDNPVILRIMRLLL QGRKVGIVTAAGYTDAAKYYERLK GLLDAMYESAEMTDAQRAGLVVMGGESNFLFRYD HASPSRLSYVPREEWLLEEMKTWQ EGDITRLLDIAESSLRACASNLPVAVLRKDRA VGVYPTERGRISREQLEETVLVVQ NTVERSEVGARLPFCAFNGGNDVFVDIGDKSWG V RACQRYFGGIEPARTLHVGDQFLS AGANDFKARLASTTAWIASPAETVQLLDELQGI"
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		/number=6
intron	complement(156319..156370)	/locus-tag="An18g01690"
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gene	complement(<156827..>15700)	/locus-tag="An18g01700"

	8638)	
mRNA	complement(join(<156827 /locus-tag="An18g01700" ..157888, 157938..158066, 158115..158310, 158364..>158638))	
CDS	complement(join(156827. /locus-tag="An18g01700" .157888,157938..158066, 158115..158310, 158364..158638))	/inference="profile:COGS:COG0477" /inference="profile:PFAM:PF00083" /note="unnamed protein product; Function: qutD of E. nidulans is involved in quinic acid transport with similarity to the maltose transport protein MAL61. Phenotype: mutations in the qutD gene of A. nidulans cause the loss of ability to grow upon quinic acid as sole carbon source in media at normal pH 6. 5 and failure to induce three enzyme activities specifically required for metabolism to protochatechuic acid. Similarity: the ORF overlaps with A. niger EST EMBLEST:BE759752. Title: strong similarity to quinate transport protein qutD - Aspergillus nidulans" /citation=[6] /citation=[10] /codon-start=1 /protein-id="CAK47242.1" /db-xref="GI:134084209" /translation="MAGSKKPVNIFRLRLADPK EVFNWRLWFAVLSFGLMGAARGVD EGLISGAFNSKDFQRTIHLDSYSEVQTNIKANV SAMVQIGSVGGALFAFLVCDRIGR LWATRQLCVLWILGIAIFMGVGANGSLGAVYAGR FVAGLGVGQTVVVGPPVYLAEIAPA SVRGLCTCVFTGFVYLGIVLAYFTNYGCQIHMGD HTHKRWEVPTSLHIMFAGLIFLLS FLQYESPRFLVKKKGKPEEALKNLARLRLNPPEHE YVVEEFTGIQNAHQAEEMATMGAG WLGIVKEAIMVPSNLYRLYLAAMAQLLSQWSGAG SITLYAPDLFSLLGITGSNESLLV TAVFGIIKLVAAVICALFLVDVIGRKRALLLGIT LQAISMIYVASFLTAVPEMGIVDD FVLPESKKGSSRGAIAMIYISGVGWALGWNSMQY LLTAEFLPLRIRALATSAAMTLHF VNQYGNRAVPNMLLGTAEGGITPKGTFWFFSAV TVLGGLWVWFVSPETAGRSLESMD RLFALPWYQIGRHGNRDADQQDQVVADKQQQVED GFGGAEHRERV"
sig-peptide	complement(158513..158638)	/locus-tag="An18g01700"
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mat-peptide	complement(join(156830. .157888,157938..158066,	/locus-tag="An18g01700"

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exon      complement(157938..158066) /locus-tag="An18g01700"
                                         /number=2
intron    complement(158067..158114) /locus-tag="An18g01700"
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exon      complement(158115..158310) /locus-tag="An18g01700"
intron    complement(158311..158363) /locus-tag="An18g01700"
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CDS        join(159975..160316, /locus-tag="An18g01720"
160367..160732,
160782..161738,
161796..161849)
                                         /inference="profile:COGS:COG0477"
                                         /note="unnamed protein product;
Function: CaMDR1 of C. albicans
the confers insensitivity to the
anti-mitotic drug, benomyl, and to
the dihydrofolate reductase
inhibitor, methotrexate. Remark:

```

seven different mutant alleles of CaMDR1 from *C. albicans* showed distinct drug resistance profiles. Similarity: the ORF shows similarity to several major facilitator proteins from different species. Title: strong similarity to benomyl/methotrexate resistance protein MDR1 - *Candida albicans* plasma membrane"

/citation=[13]

/citation=[20]

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TIIDWDDHDPENPQHWP L WKKVVVTFEICLLTF  
SVYIGSAIYSAGIESVMSEFQISQ  
VAATLGLTLFVAGYGLGPLLWSPMSEVPQIGRNS  
VYIATLIVFVALQVPAALAGNLGT  
LLAFRFLTGF FGSPALATGGASLADMFAPRKRAY  
GIGIWGISAICGPVLGPLVGGFAA  
QAKGWRWTIWELMWLSGFTLVVLIIFLPETSSSN  
ILYRRARRLRKLTNRSNLRSEPEL  
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 162961 acactacgat atagacctca ctgactttcg ccctaccctg cgtcatggca gccgatgcgg  
 163021 gattgacgac gtaagccaca tctcggaagg tttttgacat cgccgcagcc acgttgtcca  
 163081 tcgcgagga cagtcgacg gaaaggatct cactgcaccc agtaatatatt gccacggcca  
 163141 gtgcctggag cgtgtcaaaa ccagcatacc agcctttatc cagcgggtcg aaatatattt  
 163201 ccgatccgga cctagtgcgc tgaccgcaga aaatggcggt taggaaggga tagatccact  
 163261 gtttggcatc accactaagt atgaaagatt gcggggcttt gtgcacacca agatcggaac  
 163321 cccaagagtc aggggtgaga ttcaatcctg cagactgatg gacattatta gtggaagtcc  
 163381 aattatactg aaaccagatc gccgcgctct tatcactgta gttgttctgg tagactgtag  
 163441 gacgaaagct gcgcacgatg ggctccagag aacactctgt agcttcccac tgtgtgccat  
 163501 tcgtcatagg ggaatcgctg agcagctcca gggtggcccg aggggccatg tattgaattg  
 163561 caatcaatgt agcattggta taaaccaccg catcataagt ggagactggg gtcattgaaa  
 163621 aggtgctaaa tgagtaatcg tctggcatat accaggccga gagaccgctt ttcggtagt

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LOCUS (LOC): AM270325 GenBank (R)  
 GenBank ACC. NO. (GBN): AM270325  
 GenBank VERSION (VER): AM270325.1 GI:134081809  
 CAS REGISTRY NO. (RN): 928583-76-0  
 SEQUENCE LENGTH (SQL): 226503  
 MOLECULE TYPE (CI): DNA; linear  
 DIVISION CODE (CI): Plants, fungi, algae  
 DATE (DATE): 24 Mar 2007  
 DEFINITION (DEF): *Aspergillus niger* contig An14c0180, complete genome.  
 SOURCE: *Aspergillus niger*  
 ORGANISM (ORGN): *Aspergillus niger*  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina;  
 Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic  
 Trichocomaceae; *Aspergillus*  
 REFERENCE: 1 (bases 23835 to 25756)  
 AUTHOR (AU): Jones, S.W.; Luk, K.C.  
 TITLE (TI): Isolation of a chicken thioredoxin cDNA clone.  
 Thioredoxin mRNA is differentially expressed in normal  
 and Rous sarcoma virus-transformed chicken embryo  
 fibroblasts  
 JOURNAL (SO): J. Biol. Chem., 263 (20), 9607-9611 (1988)  
 OTHER SOURCE (OS): CA 109:105752  
 REFERENCE: 2 (bases 16557 to 19301)  
 AUTHOR (AU): Robinson, J.S.; Klionsky, D.J.; Banta, L.M.; Emr, S.D.  
 TITLE (TI): Protein sorting in *Saccharomyces cerevisiae*: isolation  
 of mutants defective in the delivery and processing of  
 multiple vacuolar hydrolases  
 JOURNAL (SO): Mol. Cell. Biol., 8 (11), 4936-4948 (1988)  
 OTHER SOURCE (OS): CA 110:20954  
 REFERENCE: 3 (bases 181479 to 182990)  
 AUTHOR (AU): Jackson, B.J.; Warren, C.D.; Bugge, B.; Robbins, P.W.  
 TITLE (TI): Synthesis of lipid-linked oligosaccharides in  
*Saccharomyces cerevisiae*: Man2GlcNAc2 and Man1GlcNAc2  
 are transferred from dolichol to protein in vivo  
 Arch. Biochem. Biophys., 272 (1), 203-209 (1989)  
 JOURNAL (SO): Arch. Biochem. Biophys., 272 (1), 203-209 (1989)  
 OTHER SOURCE (OS): CA 111:74550  
 REFERENCE: 4 (bases 197258 to 198879)  
 AUTHOR (AU): Szumanski, M.B.; Boyle, S.M.  
 TITLE (TI): Analysis and sequence of the *speB* gene encoding

agmatine ureohydrolase, a putrescine biosynthetic enzyme in *Escherichia coli*  
 JOURNAL (SO): J. Bacteriol., 172 (2), 538-547 (1990)  
 OTHER SOURCE (OS): CA 113:18542  
 REFERENCE: 5 (bases 8900 to 10226)  
 AUTHOR (AU): Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; Kan, Y.W.; Palek, J.  
 TITLE (TI): cDNA sequence for human erythrocyte ankyrin  
 JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 87 (5), 1730-1734 (1990)  
 OTHER SOURCE (OS): CA 113:146283  
 REFERENCE: 6 (bases 149275 to 150765)  
 AUTHOR (AU): Chen, W.N.; Balzi, E.; Capieaux, E.; Choder, M.; Goffeau, A.  
 TITLE (TI): The DNA sequencing of the 17 kb HindIII fragment spanning the LEU1 and ATE1 loci on chromosome VII from *Saccharomyces cerevisiae* reveals the PDR6 gene, a new member of the genetic network controlling pleiotropic drug resistance  
 JOURNAL (SO): Yeast, 7 (3), 287-299 (1991)  
 OTHER SOURCE (OS): CA 116:16482  
 REFERENCE: 7 (bases 20272 to 22263)  
 AUTHOR (AU): Tobias, J.W.; Varshavsky, A.  
 TITLE (TI): Cloning and functional analysis of the ubiquitin-specific protease gene UBP1 of *Saccharomyces cerevisiae*  
 JOURNAL (SO): J. Biol. Chem., 266 (18), 12021-12028 (1991)  
 OTHER SOURCE (OS): CA 116:122304  
 REFERENCE: 8 (bases 92137 to 93393)  
 AUTHOR (AU): Gosalbes, M.J.; Perez-Gonzalez, J.A.; Gonzalez, R.; Navarro, A.  
 TITLE (TI): Two beta-glycanase genes are clustered in *Bacillus polymyxa*: molecular cloning, expression, and sequence analysis of genes encoding a xylanase and an endo-beta-(1,3)-(1,4)-glucanase  
 JOURNAL (SO): J. Bacteriol., 173 (23), 7705-7710 (1991)  
 OTHER SOURCE (OS): CA 118:33731  
 REFERENCE: 9 (bases 159715 to 163074)  
 AUTHOR (AU): Kumar, V.; Ramakrishnan, S.; Teeri, T.T.; Knowles, J.K.; Hartley, B.S.  
 TITLE (TI): *Saccharomyces cerevisiae* cells secreting an *Aspergillus niger* beta-galactosidase grow on whey permeate  
 JOURNAL (SO): Biotechnology (N.Y.), 10 (1), 82-85 (1992)  
 REFERENCE: 10 (bases 197258 to 198879)  
 AUTHOR (AU): Szumanski, M.B.; Boyle, S.M.  
 TITLE (TI): Influence of cyclic AMP, agmatine, and a novel protein encoded by a flanking gene on speB (agmatine ureohydrolase) in *Escherichia coli*  
 JOURNAL (SO): J. Bacteriol., 174 (3), 758-764 (1992)  
 OTHER SOURCE (OS): CA 119:21634  
 REFERENCE: 11 (bases 16557 to 19301)  
 AUTHOR (AU): Wada, Y.; Ohsumi, Y.; Anraku, Y.  
 TITLE (TI): Genes for directing vacuolar morphogenesis in *Saccharomyces cerevisiae*. I. Isolation and characterization of two classes of vam mutants  
 JOURNAL (SO): J. Biol. Chem., 267 (26), 18665-18670 (1992)  
 OTHER SOURCE (OS): CA 117:105596  
 REFERENCE: 12 (bases 20272 to 22263)  
 AUTHOR (AU): Baker, R.T.; Tobias, J.W.; Varshavsky, A.  
 TITLE (TI): Ubiquitin-specific proteases of *Saccharomyces cerevisiae*. Cloning of UBP2 and UBP3, and functional analysis of the UBP gene family  
 JOURNAL (SO): J. Biol. Chem., 267 (32), 23364-23375 (1992)  
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AUTHOR (AU): Horazdovsky, B.F.; Emr, S.D.  
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sedimentable protein complex and is essential for  
vacuolar protein sorting in yeast  
JOURNAL (SO): J. Biol. Chem., 268 (7), 4953-4962 (1993)  
OTHER SOURCE (OS): CA 118:229898

REFERENCE: 14 (bases 32776 to 34762)  
AUTHOR (AU): Roebroek, A.J.; Creemers, J.W.; Pauli, I.G.; Bogaert, T.;  
Van de Ven, W.J.  
TITLE (TI): Generation of structural and functional diversity in  
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JOURNAL (SO): EMBO J., 12 (5), 1853-1870 (1993)  
OTHER SOURCE (OS): CA 120:70454

REFERENCE: 15 (bases 181479 to 182990)  
AUTHOR (AU): Jackson, B.J.; Kukuruzinska, M.A.; Robbins, P.  
TITLE (TI): Biosynthesis of asparagine-linked oligosaccharides in  
*Saccharomyces cerevisiae*: the *alg2* mutation  
JOURNAL (SO): Glycobiology, 3 (4), 357-364 (1993)  
OTHER SOURCE (OS): CA 120:126513

REFERENCE: 16 (bases 22652 to 23365)  
AUTHOR (AU): Errabolu, R.; Sanders, M.A.; Salisbury, J.L.  
TITLE (TI): Cloning of a cDNA encoding human centrin, an EF-hand  
protein of centrosomes and mitotic spindle poles  
JOURNAL (SO): J. Cell. Sci., 107 (PT 1), 9-16 (1994)  
OTHER SOURCE (OS): CA 122:3785

REFERENCE: 17 (bases 72683 to 73072)  
AUTHOR (AU): Ishikawa, A.; Ohta, S.; Matsuoka, K.; Hattori, T.;  
Nakamura, K.  
TITLE (TI): A family of potato genes that encode Kunitz-type  
proteinase inhibitors: structural comparisons and  
differential expression  
JOURNAL (SO): Plant Cell Physiol., 35 (2), 303-312 (1994)  
OTHER SOURCE (OS): CA 121:100855

REFERENCE: 18 (bases 149275 to 150765)  
AUTHOR (AU): Lai, M.H.; Bard, M.; Pierson, C.A.; Alexander, J.F.;  
Goebel, M.; Carter, G.T.; Kirsch, D.R.  
TITLE (TI): The identification of a gene family in the  
*Saccharomyces cerevisiae* ergosterol biosynthesis  
pathway  
JOURNAL (SO): Gene, 140 (1), 41-49 (1994)  
OTHER SOURCE (OS): CA 121:127004

REFERENCE: 19 (bases 176803 to 178484)  
AUTHOR (AU): Kil, K.S.; Cunningham, M.W.; Barnett, L.A.  
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67-kilodalton myosin-cross-reactive antigen of  
*Streptococcus pyogenes* reveals its similarity with  
class II major histocompatibility antigens  
JOURNAL (SO): Infect. Immun., 62 (6), 2440-2449 (1994)  
OTHER SOURCE (OS): CA 122:73390

REFERENCE: 20 (bases 48251 to 50618)  
AUTHOR (AU): Sato, S.; Suzuki, H.; Widyastuti, U.; Hotta, Y.; Tabata, S.  
TITLE (TI): Identification and characterization of genes induced  
during sexual differentiation in *Schizosaccharomyces*  

JOURNAL (SO): Curr. Genet., 26 (1), 31-37 (1994)  
OTHER SOURCE (OS): CA 121:197248

REFERENCE: 21 (bases 157327 to 158616)  
AUTHOR (AU): Marcus, G.A.; Silverman, N.; Berger, S.L.; Horiuchi, J.;  
Guarente, L.  
TITLE (TI): Functional similarity and physical association between

JOURNAL (SO): GCN5 and ADA2: putative transcriptional adaptors  
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 OTHER SOURCE (OS): CA 122:2700  
 REFERENCE: 22 (bases 149275 to 150765)  
 AUTHOR (AU): Lees,N.D.; Skaggs,B.; Kirsch,D.R.; Bard,M.  
 TITLE (TI): Cloning of the late genes in the ergosterol  
 biosynthetic pathway of *Saccharomyces cerevisiae*--a  
 review  
 JOURNAL (SO): Lipids, 30 (3), 221-226 (1995)  
 OTHER SOURCE (OS): CA 123:79105  
 REFERENCE: 23 (bases 157327 to 158616)  
 AUTHOR (AU): Horiuchi,J.; Silverman,N.; Marcus,G.A.; Guarente,L.  
 TITLE (TI): ADA3, a putative transcriptional adaptor, consists of  
 two separable domains and interacts with ADA2 and GCN5  
 in a trimeric complex  
 JOURNAL (SO): Mol. Cell. Biol., 15 (3), 1203-1209 (1995)  
 OTHER SOURCE (OS): CA 122:232629  
 REFERENCE: 24 (bases 41237 to 43709)  
 AUTHOR (AU): Harris,C.L.; Kolanko,C.J.  
 TITLE (TI): Aminoacyl-tRNA synthetase complex in *Saccharomyces*  
*cerevisiae*  
 JOURNAL (SO): Biochem. J., 309 (PT 1), 321-324 (1995)  
 OTHER SOURCE (OS): CA 123:106013  
 REFERENCE: 25 (bases 190148 to 191691)  
 AUTHOR (AU): Russo,M.W.; Sevetson,B.R.; Milbrandt,J.  
 TITLE (TI): Identification of NAB1, a repressor of NGFI-A- and  
 Krox20-mediated transcription  
 JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 92 (15), 6873-6877  
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 OTHER SOURCE (OS): CA 123:277433  
 REFERENCE: 26 (bases 163244 to 165037)  
 AUTHOR (AU): Saupe,S.; Turcq,B.; Begueret,J.  
 TITLE (TI): A gene responsible for vegetative incompatibility in  
 the fungus *Podospira anserina* encodes a protein with a  
 GTP-binding motif and G beta homologous domain  
 JOURNAL (SO): Gene, 162 (1), 135-139 (1995)  
 OTHER SOURCE (OS): CA 123:331620  
 REFERENCE: 27 (bases 20272 to 22263)  
 AUTHOR (AU): Hochstrasser,M.  
 TITLE (TI): Ubiquitin-dependent protein degradation  
 JOURNAL (SO): Annu. Rev. Genet., 30, 405-439 (1996)  
 OTHER SOURCE (OS): CA 126:43976  
 REFERENCE: 28 (bases 65395 to 67116)  
 AUTHOR (AU): Stearman,R.; Yuan,D.S.; Yamaguchi-Iwai,Y.;  
 Klausner,R.D.; Dancis,A.  
 TITLE (TI): A permease-oxidase complex involved in high-affinity  
 iron uptake in yeast  
 JOURNAL (SO): Science, 271 (5255), 1552-1557 (1996)  
 OTHER SOURCE (OS): CA 124:225984  
 REFERENCE: 29 (bases 157327 to 158616)  
 AUTHOR (AU): Wolffe,A.P.; Pruss,D.  
 TITLE (TI): Targeting chromatin disruption: Transcription  
 regulators that acetylate histones  
 JOURNAL (SO): Cell, 84 (6), 817-819 (1996)  
 OTHER SOURCE (OS): CA 124:251873  
 REFERENCE: 30 (bases 190148 to 191691)  
 AUTHOR (AU): Svaren,J.; Sevetson,B.R.; Apel,E.D.; Zimonjic,D.B.;  
 Milbrandt,J.  
 TITLE (TI): NAB2, a corepressor of NGFI-A (Egr-1) and Krox20, is  
 induced by proliferative and differentiative stimuli  
 JOURNAL (SO): Mol. Cell. Biol., 16 (7), 3545-3553 (1996)  
 OTHER SOURCE (OS): CA 125:106429



REFERENCE: 31 (bases 157327 to 158616)  
AUTHOR (AU): Kuo,M.H.; Brownell,J.E.; Sobel,R.E.; Ranalli,T.A.;  
Cook,R.G.; Edmondson,D.G.; Roth,S.Y.; Allis,C.D.  
TITLE (TI): Transcription-linked acetylation by Gcn5p of histones  
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JOURNAL (SO): Nature, 383 (6597), 269-272 (1996)  
OTHER SOURCE (OS): CA 125:268960

REFERENCE: 32 (bases 137703 to 138530)  
AUTHOR (AU): Bang,D.D.; Ketting,R.; de Ruijter,M.; Brandsma,J.A.;  
Verhage,R.A.; van de Putte,P.; Brouwer,J.  
TITLE (TI): Cloning of Schizosaccharomyces pombe rph16+, a gene  
homologous to the Saccharomyces cerevisiae RAD16 gene  
JOURNAL (SO): Mutat. Res., 364 (2), 57-71 (1996)  
OTHER SOURCE (OS): CA 125:294310

REFERENCE: 33 (bases 2852 to 4742)  
AUTHOR (AU): Murone,M.; Simanis,V.  
TITLE (TI): The fission yeast dmal gene is a component of the  
spindle assembly checkpoint, required to prevent septum  
formation and premature exit from mitosis if spindle  
function is compromised  
JOURNAL (SO): EMBO J., 15 (23), 6605-6616 (1996)  
OTHER SOURCE (OS): CA 126:208115

REFERENCE: 34 (bases 157327 to 158616)  
AUTHOR (AU): Chiang,Y.C.; Komarnitsky,P.; Chase,D.; Denis,C.L.  
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acetyltransferase GCN5 and the core transcriptional  
factor TFIIB  
JOURNAL (SO): J. Biol. Chem., 271 (50), 32359-32365 (1996)  
OTHER SOURCE (OS): CA 126:128325

REFERENCE: 35 (bases 98558 to 100377)  
AUTHOR (AU): Stukey,J.; Carman,G.M.  
TITLE (TI): Identification of a novel phosphatase sequence motif  
JOURNAL (SO): Protein Sci., 6 (2), 469-472 (1997)  
OTHER SOURCE (OS): CA 126:289905

REFERENCE: 36 (bases 51277 to 53277)  
AUTHOR (AU): Portman,D.S.; O'Connor,J.P.; Dreyfuss,G.  
TITLE (TI): YRA1, an essential Saccharomyces cerevisiae gene,  
encodes a novel nuclear protein with RNA annealing  
activity  
JOURNAL (SO): RNA, 3 (5), 527-537 (1997)  
OTHER SOURCE (OS): CA 127:13954

REFERENCE: 37 (bases 65395 to 67116)  
AUTHOR (AU): de Silva,D.; Davis-Kaplan,S.; Fergestad,J.; Kaplan,J.  
TITLE (TI): Purification and characterization of Fet3 protein, a  
yeast homologue of ceruloplasmin  
JOURNAL (SO): J. Biol. Chem., 272 (22), 14208-14213 (1997)  
OTHER SOURCE (OS): CA 127:77719

REFERENCE: 38 (bases 98558 to 100377)  
AUTHOR (AU): Qie,L.; Nagiec,M.M.; Baltisberger,J.A.; Lester,R.L.;  
Dickson,R.C.  
TITLE (TI): Identification of a Saccharomyces gene, LCB3, necessary  
for incorporation of exogenous long chain bases into  
sphingolipids  
JOURNAL (SO): J. Biol. Chem., 272 (26), 16110-16117 (1997)  
OTHER SOURCE (OS): CA 127:146248

REFERENCE: 39 (bases 19354 to 19996)  
AUTHOR (AU): Lussier,M.; White,A.M.; Sheraton,J.; di Paolo,T.;  
Treadwell,J.; Southard,S.B.; Horenstein,C.I.;  
Chen-Weiner,J.; Ram,A.F.; Kapteyn,J.C.; Roemer,T.W.;  
Vo,D.H.; Bondoc,D.C.; Hall,J.; Zhong,W.W.; Sdicu,A.M.;  
Davies,J.; Klis,F.M.; Robbins,P.W.; Bussey,H.  
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JOURNAL (SO): Genetics, 147 (2), 435-450 (1997)  
 OTHER SOURCE (OS): CA 127:327291  
 REFERENCE: 40 (bases 65395 to 67116)  
 AUTHOR (AU): Yuan,D.S.; Dancis,A.; Klausner,R.D.  
 TITLE (TI): Restriction of copper export in *Saccharomyces cerevisiae* to a late Golgi or post-Golgi compartment in the secretory pathway

JOURNAL (SO): J. Biol. Chem., 272 (41), 25787-25793 (1997)  
 OTHER SOURCE (OS): CA 127:343694  
 REFERENCE: 41 (bases 183872 to 189440)  
 AUTHOR (AU): Wood,K.W.; Sakowicz,R.; Goldstein,L.S.; Cleveland,D.W.  
 TITLE (TI): CENP-E is a plus end-directed kinetochore motor required for metaphase chromosome alignment

JOURNAL (SO): Cell, 91 (3), 357-366 (1997)  
 OTHER SOURCE (OS): CA 128:45048  
 REFERENCE: 42 (bases 16557 to 19301)  
 AUTHOR (AU): Rieder,S.E.; Emr,S.D.  
 TITLE (TI): A novel RING finger protein complex essential for a late step in protein transport to the yeast vacuole

JOURNAL (SO): Mol. Biol. Cell, 8 (11), 2307-2327 (1997)  
 OTHER SOURCE (OS): CA 128:32213  
 REFERENCE: 43 (bases 218542 to 219708)  
 AUTHOR (AU): Nakamura,T.; Ohmoto,T.; Hirata,D.; Tsuchiya,E.; Miyakawa,T.  
 TITLE (TI): Yeast Crv4/Ttp1, a predicted type II membrane protein, is involved in an event important for growth, functionally overlapping with the event regulated by calcineurin- and Mpk1-mediated pathways

JOURNAL (SO): Mol. Gen. Genet., 256 (5), 481-487 (1997)  
 OTHER SOURCE (OS): CA 128:138463  
 REFERENCE: 44 (bases 163244 to 165037)  
 AUTHOR (AU): Espagne,E.; Balhadere,P.; Begueret,J.; Turcq,B.  
 TITLE (TI): Reactivity in vegetative incompatibility of the HET-E protein of the fungus *Podospora anserina* is dependent on GTP-binding activity and a WD40 repeated domain

JOURNAL (SO): Mol. Gen. Genet., 256 (6), 620-627 (1997)  
 OTHER SOURCE (OS): CA 128:214667  
 REFERENCE: 45 (bases 98558 to 100377)  
 AUTHOR (AU): Mao,C.; Wadleigh,M.; Jenkins,G.M.; Hannun,Y.A.; Obeid,L.M.  
 TITLE (TI): Identification and characterization of *Saccharomyces cerevisiae* dihydrosphingosine-1-phosphate phosphatase

JOURNAL (SO): J. Biol. Chem., 272 (45), 28690-28694 (1997)  
 OTHER SOURCE (OS): CA 128:72216  
 REFERENCE: 46 (bases 103137 to 103945)  
 AUTHOR (AU): Kondoh,O.; Tachibana,Y.; Ohya,Y.; Arisawa,M.; Watanabe,T.  
 TITLE (TI): Cloning of the RH01 gene from *Candida albicans* and its regulation of beta-1,3-glucan synthesis

JOURNAL (SO): J. Bacteriol., 179 (24), 7734-7741 (1997)  
 OTHER SOURCE (OS): CA 128:111391  
 REFERENCE: 47 (bases 67552 to 68735)  
 AUTHOR (AU): Gonzalez,F.J.; Montes,J.; Martin,F.; Lopez,M.C.; Ferminan,E.; Catalan,J.; Galan,M.A.; Dominguez,A.  
 TITLE (TI): Molecular cloning of TvDAO1, a gene encoding a D-amino acid oxidase from *Trigonopsis variabilis* and its expression in *Saccharomyces cerevisiae* and *Kluyveromyces lactis*

JOURNAL (SO): Yeast, 13 (15), 1399-1408 (1997)  
 OTHER SOURCE (OS): CA 128:150109

REFERENCE: 48 (bases 41237 to 43709)  
AUTHOR (AU): Motorin, Y.; Le Caer, J.P.; Waller, J.P.  
TITLE (TI): Cysteinyl-tRNA synthetase from *Saccharomyces cerevisiae*. Purification, characterization and assignment to the genomic sequence YNL247w  
JOURNAL (SO): *Biochimie*, 79 (12), 731-740 (1997)  
OTHER SOURCE (OS): CA 129:24853

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AUTHOR (AU): Mandala, S.M.; Thornton, R.; Tu, Z.; Kurtz, M.B.; Nickels, J.; Broach, J.; Menzeleev, R.; Spiegel, S.  
TITLE (TI): Sphingoid base 1-phosphate phosphatase: a key regulator of sphingolipid metabolism and stress response  
JOURNAL (SO): *Proc. Natl. Acad. Sci. U.S.A.*, 95 (1), 150-155 (1998)  
OTHER SOURCE (OS): CA 128:151503

REFERENCE: 50 (bases 65395 to 67116)  
AUTHOR (AU): Gaxiola, R.A.; Yuan, D.S.; Klausner, R.D.; Fink, G.R.  
TITLE (TI): The yeast CLC chloride channel functions in cation homeostasis  
JOURNAL (SO): *Proc. Natl. Acad. Sci. U.S.A.*, 95 (7), 4046-4050 (1998)  
OTHER SOURCE (OS): CA 128:319139

REFERENCE: 51 (bases 151141 to 153445)  
AUTHOR (AU): Cazelle, B.; Pokorska, A.; Hull, E.; Green, P.M.; Stanway, G.; Scazzocchio, C.  
TITLE (TI): Sequence, exon-intron organization, transcription and mutational analysis of *prnA*, the gene encoding the transcriptional activator of the *prn* gene cluster in *Aspergillus nidulans*  
JOURNAL (SO): *Mol. Microbiol.*, 28 (2), 355-370 (1998)  
OTHER SOURCE (OS): CA 129:63816

REFERENCE: 52 (bases 48251 to 50618)  
AUTHOR (AU): Lubkowitz, M.A.; Barnes, D.; Breslav, M.; Burchfield, A.; Naider, F.; Becker, J.M.  
TITLE (TI): *Schizosaccharomyces pombe* *isp4* encodes a transporter representing a novel family of oligopeptide transporters  
JOURNAL (SO): *Mol. Microbiol.*, 28 (4), 729-741 (1998)  
OTHER SOURCE (OS): CA 129:119284

REFERENCE: 53 (bases 54264 to 55012)  
AUTHOR (AU): Babst, M.; Wendland, B.; Estepa, E.J.; Emr, S.D.  
TITLE (TI): The Vps4p AAA ATPase regulates membrane association of a Vps protein complex required for normal endosome function  
JOURNAL (SO): *EMBO J.*, 17 (11), 2982-2993 (1998)  
OTHER SOURCE (OS): CA 129:146701

REFERENCE: 54 (bases 149275 to 150765)  
AUTHOR (AU): Silve, S.; Dupuy, P.H.; Ferrara, P.; Loison, G.  
TITLE (TI): Human lamin B receptor exhibits sterol C14-reductase activity in *Saccharomyces cerevisiae*  
JOURNAL (SO): *Biochim. Biophys. Acta*, 1392 (2-3), 233-244 (1998)  
OTHER SOURCE (OS): CA 129:146116

REFERENCE: 55 (bases 27949 to 28578)  
AUTHOR (AU): Caldas, C.; Kim, M.H.; MacGregor, A.; Cain, D.; Aparicio, S.; Wiedemann, L.M.  
TITLE (TI): Isolation and characterization of a pufferfish MLL (mixed lineage leukemia)-like gene (*fMll*) reveals evolutionary conservation in vertebrate genes related to *Drosophila trithorax*  
JOURNAL (SO): *Oncogene*, 16 (25), 3233-3241 (1998)  
OTHER SOURCE (OS): CA 129:171330

REFERENCE: 56 (bases 218542 to 219708)  
AUTHOR (AU): Rayner, J.C.; Munro, S.  
TITLE (TI): Identification of the MNN2 and MNN5

mannosyltransferases required for forming and extending the mannose branches of the outer chain mannans of *Saccharomyces cerevisiae*  
JOURNAL (SO): J. Biol. Chem., 273 (41), 26836-26843 (1998)  
OTHER SOURCE (OS): CA 130:22764  
REFERENCE: 57 (bases 218542 to 219708)  
AUTHOR (AU): Lussier,M.; Sdicu,A.M.; Bussey,H.  
TITLE (TI): The KTR and MNN1 mannosyltransferase families of *Saccharomyces cerevisiae*

JOURNAL (SO): Biochim. Biophys. Acta, 1426 (2), 323-334 (1999)  
OTHER SOURCE (OS): CA 130:293055  
REFERENCE: 58 (bases 154037 to 156562)  
AUTHOR (AU): de Vries,R.P.; Visser,J.; de Graaff,L.H.  
TITLE (TI): CreA modulates the XlnR-induced expression on xylose of *Aspergillus niger* genes involved in xylan degradation

JOURNAL (SO): Res. Microbiol., 150 (4), 281-285 (1999)  
OTHER SOURCE (OS): CA 131:180701  
REFERENCE: 59 (bases 80610 to 81592)  
AUTHOR (AU): Ui,S.; Mimura,A.; Ohkuma,M.; Kudo,T.  
TITLE (TI): Formation of a chiral acetoinic compound from diacetyl by *Escherichia coli* expressing meso-2,3-butanediol dehydrogenase

JOURNAL (SO): Lett. Appl. Microbiol., 28 (6), 457-460 (1999)  
OTHER SOURCE (OS): CA 131:225912  
REFERENCE: 60 (bases 211445 to 212528)  
AUTHOR (AU): Krappmann,S.; Helmstaedt,K.; Gerstberger,T.; Eckert,S.; Hoffmann,B.; Hoppert,M.; Schnappauf,G.; Braus,G.H.  
TITLE (TI): The *aroC* gene of *Aspergillus nidulans* codes for a monofunctional, allosterically regulated chorismate mutase

JOURNAL (SO): J. Biol. Chem., 274 (32), 22275-22282 (1999)  
OTHER SOURCE (OS): CA 131:268796  
REFERENCE: 61 (bases 137703 to 138530)  
AUTHOR (AU): Lombaerts,M.; Peltola,P.H.; Visse,R.; den Dulk,H.; Brouwer,J.  
TITLE (TI): Characterization of the *rhp7(+)* and *rhp16(+)* genes in *Schizosaccharomyces pombe*

JOURNAL (SO): Nucleic Acids Res., 27 (17), 3410-3416 (1999)  
OTHER SOURCE (OS): CA 132:809  
REFERENCE: 62  
AUTHOR (AU): Tsai,H.F.; Wheeler,M.H.; Chang,Y.C.; Kwon-Chung,K.J.  
TITLE (TI): A developmentally regulated gene cluster involved in conidial pigment biosynthesis in *Aspergillus fumigatus*

JOURNAL (SO): J. Bacteriol., 181 (20), 6469-6477 (1999)  
OTHER SOURCE (OS): CA 132:45624  
REFERENCE: 63  
AUTHOR (AU): DeZwaan,T.M.; Carroll,A.M.; Valent,B.; Sweigard,J.A.  
TITLE (TI): *Magnaporthe grisea* *pth11p* is a novel plasma membrane protein that mediates appressorium differentiation in response to inductive substrate cues

JOURNAL (SO): Plant Cell, 11 (10), 2013-2030 (1999)  
OTHER SOURCE (OS): CA 132:47358  
REFERENCE: 64 (bases 20272 to 22263)  
AUTHOR (AU): Layfield,R.; Franklin,K.; Landon,M.; Walker,G.; Wang,P.; Ramage,R.; Brown,A.; Love,S.; Urquhart,K.; Muir,T.; Baker,R.; Mayer,R.J.  
TITLE (TI): Chemically synthesized ubiquitin extension proteins detect distinct catalytic capacities of deubiquitinating enzymes

JOURNAL (SO): Anal. Biochem., 274 (1), 40-49 (1999)  
OTHER SOURCE (OS): CA 132:20406  
REFERENCE: 65 (bases 55690 to 56601)

AUTHOR (AU): Munoz,M.J.; Bejarano,E.R.; Daga,R.R.; Jimenez,J.  
TITLE (TI): The identification of Wos2, a p23 homologue that interacts with Wee1 and Cdc2 in the mitotic control of fission yeasts  
JOURNAL (SO): Genetics, 153 (4), 1561-1572 (1999)  
OTHER SOURCE (OS): CA 132:177833  
REFERENCE: 66 (bases 149275 to 150765)  
AUTHOR (AU): Zweytick,D.; Hrastnik,C.; Kohlwein,S.D.; Daum,G.  
TITLE (TI): Biochemical characterization and subcellular localization of the sterol C-24(28) reductase, erg4p, from the yeast saccharomyces cerevisiae  
JOURNAL (SO): FEBS Lett., 470 (1), 83-87 (2000)  
OTHER SOURCE (OS): CA 132:331762  
REFERENCE: 67 (bases 51277 to 53277)  
AUTHOR (AU): Cole,C.N.  
TITLE (TI): mRNA export: the long and winding road  
JOURNAL (SO): Nat. Cell Biol., 2 (4), E55-E58 (2000)  
OTHER SOURCE (OS): CA 133:27711  
REFERENCE: 68 (bases 51277 to 53277)  
AUTHOR (AU): Stutz,F.; Bachi,A.; Doerks,T.; Braun,I.C.; Seraphin,B.; Wilm,M.; Bork,P.; Izaurralde,E.  
TITLE (TI): REF, an evolutionary conserved family of hnRNP-like proteins, interacts with TAP/Mex67p and participates in mRNA nuclear export  
JOURNAL (SO): RNA, 6 (4), 638-650 (2000)  
OTHER SOURCE (OS): CA 133:70318  
REFERENCE: 69 (bases 163244 to 165037)  
AUTHOR (AU): Loubradou,G.; Turcq,B.  
TITLE (TI): Vegetative incompatibility in filamentous fungi: a roundabout way of understanding the phenomenon  
JOURNAL (SO): Res. Microbiol., 151 (4), 239-245 (2000)  
OTHER SOURCE (OS): CA 133:234784  
REFERENCE: 70 (bases 166037 to 167516)  
AUTHOR (AU): Yu,J.; Woloshuk,C.P.; Bhatnagar,D.; Cleveland,T.E.  
TITLE (TI): Cloning and characterization of avfA and omtB genes involved in aflatoxin biosynthesis in three Aspergillus species  
JOURNAL (SO): Gene, 248 (1-2), 157-167 (2000)  
OTHER SOURCE (OS): CA 133:345391  
REFERENCE: 71 (bases 143978 to 145355)  
AUTHOR (AU): Sanders,P.M.; Lee,P.Y.; Biesgen,C.; Boone,J.D.; Beals,T.P.; Weiler,E.W.; Goldberg,R.B.  
TITLE (TI): The arabidopsis DELAYED DEHISCENCE1 gene encodes an enzyme in the jasmonic acid synthesis pathway  
JOURNAL (SO): Plant Cell, 12 (7), 1041-1061 (2000)  
OTHER SOURCE (OS): CA 134:25937  
REFERENCE: 72 (bases 145510 to 146577)  
AUTHOR (AU): Cheng,Q.; Thomas,S.M.; Kostichka,K.; Valentine,J.R.; Nagarajan,V.  
TITLE (TI): Genetic analysis of a gene cluster for cyclohexanol oxidation in Acinetobacter sp. Strain SE19 by in vitro transposition  
JOURNAL (SO): J. Bacteriol., 182 (17), 4744-4751 (2000)  
OTHER SOURCE (OS): CA 134:37832  
REFERENCE: 73 (bases 163244 to 165037)  
AUTHOR (AU): Saupe,S.J.  
TITLE (TI): Molecular genetics of heterokaryon incompatibility in filamentous ascomycetes  
JOURNAL (SO): Microbiol. Mol. Biol. Rev., 64 (3), 489-502 (2000)  
OTHER SOURCE (OS): CA 134:27321  
REFERENCE: 74 (bases 128987 to 130729)  
AUTHOR (AU): Tanaka,A.; Tsuge,T.

TITLE (TI): Structural and functional complexity of the genomic region controlling AK-toxin biosynthesis and pathogenicity in the Japanese pear pathotype of *Alternaria alternata*  
 JOURNAL (SO): Mol. Plant Microbe Interact., 13 (9), 975-986 (2000)  
 OTHER SOURCE (OS): CA 134:96037  
 REFERENCE: 75 (bases 143978 to 145355)  
 AUTHOR (AU): Stintzi,A.; Browse,J.  
 TITLE (TI): The Arabidopsis male-sterile mutant, *opr3*, lacks the 12-oxophytodienoic acid reductase required for jasmonate synthesis  
 JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 97 (19), 10625-10630 (2000)  
 OTHER SOURCE (OS): CA 133:293530  
 REFERENCE: 76 (bases 54264 to 55012)  
 AUTHOR (AU): Amerik,A.Y.; Nowak,J.; Swaminathan,S.; Hochstrasser,M.  
 TITLE (TI): The Doa4 deubiquitinating enzyme is functionally linked to the vacuolar protein-sorting and endocytic pathways  
 JOURNAL (SO): Mol. Biol. Cell, 11 (10), 3365-3380 (2000)  
 OTHER SOURCE (OS): CA 134:82296  
 REFERENCE: 77 (bases 208451 to 210658)  
 AUTHOR (AU): Tieu,Q.; Nunnari,J.  
 TITLE (TI): Mdvlp is a WD repeat protein that interacts with the dynamin-related GTPase, Dnm1p, to trigger mitochondrial division  
 JOURNAL (SO): J. Cell Biol., 151 (2), 353-366 (2000)  
 OTHER SOURCE (OS): CA 134:52741  
 REFERENCE: 78 (bases 208451 to 210658)  
 AUTHOR (AU): Mozdy,A.D.; McCaffery,J.M.; Shaw,J.M.  
 TITLE (TI): Dnm1p GTPase-mediated mitochondrial fission is a multi-step process requiring the novel integral membrane component Fis1p  
 JOURNAL (SO): J. Cell Biol., 151 (2), 367-380 (2000)  
 OTHER SOURCE (OS): CA 134:52934  
 REFERENCE: 79 (bases 94126 to 97982)  
 AUTHOR (AU): Kadoya,T.; Kishida,S.; Fukui,A.; Hinoi,T.; Michiue,T.; Kikuchi,A.  
 TITLE (TI): Inhibition of Wnt signaling pathway by a novel axin-binding protein  
 JOURNAL (SO): J. Biol. Chem., 275 (47), 37030-37037 (2000)  
 OTHER SOURCE (OS): CA 134:233219  
 REFERENCE: 80 (bases 80610 to 81592)  
 AUTHOR (AU): Ui,S.; Takusagawa,Y.; Ohtsuki,T.; Mimura,A.; Ohkuma,M.; Kudo,T.  
 TITLE (TI): Stereochemical applications of the expression of the L-2,3-butanediol dehydrogenase gene in *Escherichia coli*  
 JOURNAL (SO): Lett. Appl. Microbiol., 32 (2), 93-98 (2001)  
 OTHER SOURCE (OS): CA 135:353434  
 REFERENCE: 81 (bases 80610 to 81592)  
 AUTHOR (AU): Otagiri,M.; Kurisu,G.; Ui,S.; Takusagawa,Y.; Ohkuma,M.; Kudo,T.; Kusunoki,M.  
 TITLE (TI): Crystal structure of meso-2,3-butanediol dehydrogenase in a complex with NAD<sup>+</sup> and inhibitor mercaptoethanol at 1.7 Å resolution for understanding of chiral substrate recognition mechanisms  
 JOURNAL (SO): J. Biochem., 129 (2), 205-208 (2001)  
 OTHER SOURCE (OS): CA 135:2180  
 REFERENCE: 82 (bases 41237 to 43709)  
 AUTHOR (AU): Davidson,E.; Caffarella,J.; Vitseva,O.; Hou,Y.M.; King,M.P.  
 TITLE (TI): Isolation of two cDNAs encoding functional human cytoplasmic cysteinyl-tRNA synthetase

JOURNAL (SO): Biol. Chem., 382 (3), 399-406 (2001)  
 OTHER SOURCE (OS): CA 135:118589  
 REFERENCE: 83 (bases 119272 to 121189)  
 AUTHOR (AU): Cukovic,D.; Ehlting,J.; VanZiffle,J.A.; Douglas,C.J.  
 TITLE (TI): Structure and evolution of 4-coumarate:coenzyme A  
 ligase (4CL) gene families  
 JOURNAL (SO): Biol. Chem., 382 (4), 645-654 (2001)  
 OTHER SOURCE (OS): CA 136:145906  
 REFERENCE: 84 (bases 87776 to 89339)  
 AUTHOR (AU): Gassama-Diagne,A.; Hullin-Matsuda,F.; Li,R.Y.;  
 Nauze,M.; Ragab,A.; Pons,V.; Delagebeaudeuf,C.;  
 Simon,M.F.; Fauvel,J.; Chap,H.  
 TITLE (TI): Enterophilins, a new family of leucine zipper proteins  
 bearing a b30.2 domain and associated with enterocyte  
 differentiation  
 JOURNAL (SO): J. Biol. Chem., 276 (21), 18352-18360 (2001)  
 OTHER SOURCE (OS): CA 136:114413  
 REFERENCE: 85 (bases 80610 to 81592)  
 AUTHOR (AU): Otagiri,M.; Kurisu,G.; Swaminathan,S.; Ui,S.;  
 Yoneda,S.; Ohkuma,M.; Kudo,T.; Kusunoki,M.  
 TITLE (TI): Crystallization and preliminary X-ray studies of  
 meso-2,3-butanediol dehydrogenase from *Klebsiella*  
*pneumoniae* IAM1063  
 JOURNAL (SO): Acta Crystallogr. D Biol. Crystallogr., 57 (PT 6),  
 857-859 (2001)  
 REFERENCE: 86 (bases 51277 to 53277)  
 AUTHOR (AU): Zenklusen,D.; Vinciguerra,P.; Strahm,Y.; Stutz,F.  
 TITLE (TI): The yeast hnRNP-Like proteins Yralp and Yra2p  
 participate in mRNA export through interaction with  
 Mex67p  
 JOURNAL (SO): Mol. Cell. Biol., 21 (13), 4219-4232 (2001)  
 OTHER SOURCE (OS): CA 135:177841  
 REFERENCE: 87 (bases 1 to 226503)  
 AUTHOR (AU): Pel,H.J.; de Winde,J.H.; Archer,D.B.; Dyer,P.S.;  
 Hofmann,G.; Schaap,P.J.; Turner,G.; de Vries,R.P.;  
 Albang,R.; Albermann,K.; Andersen,M.R.; Bendtsen,J.D.;  
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 Caddick,M.X.; Contreras,R.; Cornell,M.; Coutinho,P.M.;  
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 Heijden,R.T.; van der Kaaij,R.M.; Klis,F.M.;  
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 Lu,X.; van der Maarel,M.J.; Meulenberg,R.; Menke,H.;  
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 Pal,K.; van Peij,N.N.; Ram,A.F.; Rinas,U.; Roubos,J.A.;  
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 Vervecken,W.; van de Vondervoort,P.J.; Wedler,H.;  
 Wosten,H.A.; Zeng,A.P.; van Ooyen,A.J.; Visser,J.;  
 Stam,H.  
 TITLE (TI): Genome sequencing and analysis of the versatile cell  
 factory *Aspergillus niger* CBS 513.88  
 JOURNAL (SO): Nat. Biotechnol., 25 (2), 221-231 (2007)  
 OTHER SOURCE (OS): CA 146:310276  
 REFERENCE: 88 (bases 1 to 226503)  
 AUTHOR (AU): Pel,H.J.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (01-MAY-2006) Pel H.J., DSM, 624-0295, P.O.  
 Box 1, 2600 MA Delft, THE NETHERLANDS

## FEATURES (FEAT):

Feature Key	Location	Qualifier
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intron	1324..1419	/locus-tag="An14g05040" /number=1
exon	1420..1491	/locus-tag="An14g05040" /number=2
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intron	4086..4148	/locus-tag="An14g05050"
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intron	complement(6782..6839)	/locus-tag="An14g05070"
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intron	complement(7161..7214)	/locus-tag="An14g05070"
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 number of functionally diverse  
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 function remains unknown.  
 Similarity: the similarity to  
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 Title: weak similarity to ankyrin  
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		QLTFFVDGFIKRGVERGWFNAPGASQMQAQLNSL
		MDAYGKMETIKLTPIPAHLIHQK
		QVLALFGCVLPFGMVDDMGWWTVPMSLVIFTLY
		GIEGIGSQLEDPFQYDRNDIKMDA
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intron	12996..13053	/locus-tag="An14g05100"
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CDS	13882..14418	/locus-tag="An14g05110"
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		sequence:UniProtKB:BT004329.1"
		/note="unnamed protein product;
		Similarity: the predicted ORF
		contains an EF-hand,the most
		common domain responsible for
		calcium binding in proteins like
		calmodulin, myosin regulatory
		light chains,parvalbumins,
		troponins C, and neuronal calcium
		sensors. Title: weak similarity to
		hypothetical protein AT4g01140 -
		Arabidopsis thaliana"
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		/protein-id="CAK42072.1"
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		/translation="MNLLPLLLTLTTFLLPPIATA
		FTSTFENCQNLNRLNQTVHRVHPL
		LEKFSSIHASQSQSSTTTTTTTLANGTTITVTNTT
		SSAAIEKIEGVKALLLSSQEKIYG
		RLSNCSSDAVSPRNVLEKGVKRDDDDDGSCCTLND
		VLDQLVDTLECVLSFATGLLETIL
		DGLFDLLKTIIEGVEKLL"

sig-peptide	13882..13941	/locus-tag="An14g05110" /inference="protein motif:SignalP:2.0"
mat-peptide	13942..14415	/locus-tag="An14g05110" /product="unnamed"
exon	13882..14418	/locus-tag="An14g05110" /number=1
gene	complement(<14885..>16307)	/locus-tag="An14g05120"
mRNA	complement(join(<14885.. .15101,15159..15313, 15370..15531, 15585..15698, 15751..15900, 15955..16104, 16161..>16307))	/locus-tag="An14g05120"
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exon	complement(14885..15101)	/locus-tag="An14g05120"
intron	)	/number=1
	complement(15102..15158)	/locus-tag="An14g05120"
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exon complement(16161..16307 /locus-tag="An14g05120"
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gene <16557..>19301 /locus-tag="An14g05130"
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16910..17038,
17088..17676,
17726..18996,
19053..>19301)
CDS join(16557..16701, /locus-tag="An14g05130"
16758..16864,
16910..17038,
17088..17676,
17726..18996,
19053..19301)

/inference="profile:PFAM:PF04840"
/inference="profile:PFAM:PF04841"
/note="unnamed protein product;
Complex: VPS16 of S. cerevisiae is
a component of the so called class
C Vps complex, required for
vacuolar protein sorting and
morphology. Function: VPS16 of S.
cerevisiae is required for
vacuolar protein sorting and
vacuolar biogenesis and stability.
Phenotype: S. cerevisiae VPS16
mutants have pleiotropic defects
in vacuolar morphology and
vacuolar protein targeting. Title:
strong similarity to vacuolar
protein sorting-associated protein

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Vps16 - *Saccharomyces cerevisiae*  
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 HINRINWEYGTIRGLGWSKDEELL  
 VITEDGTVRRYFGLHGDFTSFSLGNGAEDYGVR  
 CRFWTSGFVALLSNNQLVAVSNYD  
 EPRRLLAPCEGEVSSWSLIPPAYTLRSVEVL  
 LAVDKTVYLVDPTEAEDKVLQNGP  
 FKHASVSPTGRFVALITAEGKVWVVSDFQSKYS  
 EYDPESRVTPRTVDWCGDDAVVIA  
 WEDEVHLIGPNGVAARYYYDGTVHVVEFDGVR  
 ITNDTCEFLHKVVDVTEAIFRLGS  
 TSPASVLLDSIDLLEKKSPKADENIQRIRPSLPE  
 AVDTCVKAAGHEFDYQKRLKKA  
 ASFGKSVLDLYNSDEFVEMTEKLRVLKAVRDYQI  
 GLPLSYEQYMRLTPERLIERLVNR  
 HEYLLAIRISEYLELPADRIYVHWASQKVKVSTV  
 DDDAVCKLIVQRLEGKPGISFELI  
 AQTAYDEGRAHLATQLLNHEPRAGKQVPLLLDME  
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 LKTKLPLASFFRTINTRPMASALVETTARGQDTE  
 LLKDLFYQDDRPIDGSNVLLSEAL  
 DATDLPRKTEKLQLASRLSDSKDPSVVLQKLL  
 NEASQLLKVQEALDKDLADRSEFL  
 GLSLNETIYRLIRSGYGKRAQKIQSEFRMPEKTF  
 WWLRLRALVAKRDWGELEEIGKNK  
 KSPIGWEPFYNEILGAGNTKLASLFVPKCTNLPA  
 EDKMEMWVKCGMIAKAGEEAFRAK  
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exon	16557..16701	/locus-tag="An14g05130" /number=1
intron	16702..16757	/locus-tag="An14g05130" /number=1
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intron	18997..19052	/locus-tag="An14g05130" /number=5
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gene	complement (<19354..>19996)	/locus-tag="An14g05140"

mRNA	complement(join(<19354..19554,19615..19907,19981..>19996))	/locus-tag="An14g05140"
CDS	complement(join(19354..19554,19615..19907,19981..19996))	/locus-tag="An14g05140"
		/note="unnamed protein product; Phenotype: ECM1 mutation in S. cerevisiae causes perturbation of the cell surface. Remark: ECM1 of S. cerevisiae is also called YAL059w. Title: similarity to Ecml - Saccharomyces cerevisiae" /citation=[39] /codon-start=1 /protein-id="CAK42075.1" /db-xref="GI:134081820" /translation="MAKSRPQSKHSRAARRAASP SLDVDKSLTSLPRAEETTVQRDSI LSERANAGVSKKQSKGKAKTRAQRLRQQKVERA EAVMDQLEKKVTKSEVRAKSVKAR RAEWEDLNRKTKSMFEALNEEADDNMDDAMVDDA AASKPAKRSKPAPVTQTPVVEEHE GIDVDDDDIT"
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intron	complement(19908..19980)	/locus-tag="An14g05140"
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exon	complement(19981..19996)	/locus-tag="An14g05140"
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gene	<20272..>22263	/locus-tag="An14g05150"
mRNA	<20272..>22263	/locus-tag="An14g05150"
CDS	20272..22263	/locus-tag="An14g05150" /EC-number="3.1.2.15" /inference="profile:COGS:COG5533" /inference="profile:COGS:COG5560" /inference="profile:PFAM:PF00443" /inference="similar to AA sequence:PIR:S67665" /note="unnamed protein product; Catalytic activity: ubiquitin C-terminal thiolester + H2O = ubiquitin + thiol. Function: UBP1 of S. cerevisiae has an ATP-independent isopeptidase activity, cleaving at the carboxyl terminus of the ubiquitin moiety in natural or engineered linear fusion proteins, irrespective of their size or the presence of an amino-terminal extension to ubiquitin. Similarity: UBP1 belongs to peptidase family C19;



also known as family 2 of ubiquitin carboxyl-terminal hydrolases. Similarity: although the predicted ORF is shorter than Ubp1 of *S. cerevisiae* and the alignment contains several gaps, it shows consistent similarity to several ubiquitin-specific processing proteases. Title: similarity to ubiquitin specific protease Ubp1 - *Saccharomyces cerevisiae*"

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 NNVPGLGNWDNSCYQNSIIQGLA  
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 LNSADSNQRLWTPADLKSMSWQ  
 QQDAQEYFSKIVDQLDLEVQQATRRHTRNLGLKM  
 AGPQEHVIGSGISQELQESSAGET  
 RITGNQIFRNPLEGLLAQRVGCIQCGWTEGLSLI  
 PFNCLTVPLGPKFEYDIRECLHHY  
 MHLEPIEGVECAKCTLLRVQSQLLNLLKQIGDDE  
 ETPSATPESPKISDALRSSAQERL  
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 RQAVVARPPQCLVIHVNRSMFDEN  
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 SLEAWETNPVSVSMLSHAGRGANAG  
 GHYQLRAVITHYGRHENGHYICYRKYPTDTFPAH  
 VPDAlIEADGDKERDERWYRLSDE  
 DVQMVSEANVMSQGGAFMLFYEAVEDYSPEAAED  
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 MSDVD"

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mRNA	complement(join(<22652..23018,23085..23287,23363..>23365))	/locus-tag="An14g05160"
CDS	complement(join(22652..23018,23085..23287,23363..23365))	/locus-tag="An14g05160"

/inference="profile:COGS:COG5126"  
 /inference="similar to AA  
 sequence:PIR:I38424"  
 /note="unnamed protein product;  
 Function: centrin is a ubiquitous  
 component of centrosomes and  
 mitotic spindle poles of diverse  
 organisms and plays a role in

centrosome separation at the time of mitosis. Localization: human centrin is localized at the centrosome of interphase cells and redistributes to the region of the spindle poles during mitosis. Similarity: in the predicted ORF the EF-hands are not well conserved; this fact might have important functional consequences. Similarity: the human centrin sequence has four putative calcium-binding domains as defined by the EF-hand consensus. Title: similarity to centrin - Homo sapiens centrosome"

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AVAAAKLRSRSDDAMAAEVDAAAYRLFTRGSGGVI  
TLNHLRRIARELKEEELGDELLKD  
MILEANGGAGVHAGVTLEQFHDVMTRAGVF"

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exon complement(23085..23287 /locus-tag="An14g05160"  
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intron complement(23288..23362 /locus-tag="An14g05160"  
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exon complement(23363..23365 /locus-tag="An14g05160"  
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gene <23835..>25756 /locus-tag="An14g05170"  
mRNA join(<23835..23848, /locus-tag="An14g05170"  
23890..23947,  
24000..24221,  
24272..>25756)

CDS join(23835..23848, /locus-tag="An14g05170"  
23890..23947,  
24000..24221,  
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/EC-number="1.-.-.-"  
/inference="profile:COGS:COG3118"  
/inference="profile:PFAM:PF00085"  
/note="unnamed protein product;  
Function: thioredoxin participates  
in various redox reactions through  
the reversible oxidation of its  
active center dithiol to a  
disulfide, and catalyzes  
dithiol-disulfide exchange  
reactions. Similarity: the main

feature of the predicted ORF, as well as of the very similar N. crassa hypothetical protein 17E5.270, is to contain different structural domains, including the thioredoxin and the leucine zippers in the C-terminal region. Similarity: the similarity to chicken thioredoxin and similar proteins of other species is limited to a single domain of the predicted ORF. Title: similarity to thioredoxin - Gallus gallus"

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NGVEYYFGQGIQTAIPGSTHHGQPMKHLHLGKTE  
LPLDVIEEYIQSLAEIYTPESYDL  
FLHNCNNFTQDLAMFALGKGIPHEHIQNLPQTFLS  
TPFGQMMKPQIEMALRGVTQGTGA  
GTGTVGTQTPTTSAPTAPAQPAPVTQGSVRIASN  
LAQLEHHLAAAADSCAVIFFTSAT  
CPPCKMVYPTYDELAEEAGAKATLIKVDISTAMD  
VSMKYSVRATPTFMTFLKGQKLDE  
WSGANPAQLRGNVRLLEMAHPPHRHQQLRLPSL  
QRPITNYVTYKKVPPLDKLVQKLD  
PHHEDPRLLSMITYLKHRTSSSTPAADTPLPQDL  
PSFATYLTTCGFLALDHLFALVD  
LTRLLFLDPRVSGYFAEEP GHTTLLTLLSPSAGL  
SGCPYNLRIVMLQLCCTLFSTPLY  
RDQLTTSSSLPTLLHLTTSSLLDSHTNLRVVAA  
SLAYNLAALNHNARFAGHADPLSE  
ESQVELTASLVEAITQEEESQEALHGLLFALGLL  
VYEASPD SAVVDLCKAMGIAETVA  
AKRNVEKVAKEPLIKEVGEELLMKGL"

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intron	23849..23889
exon	23890..23947
intron	23948..23999
exon	24000..24221
intron	24222..24271
exon	24272..25756
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CDS	27298..27621

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mRNA	complement(<27949..>28578)	/locus-tag="An14g05190"
CDS	complement(27949..28578)	/locus-tag="An14g05190"
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exon	complement(27949..28578)	/locus-tag="An14g05190"
		/number=1
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mRNA	join(<28642..28681, 28733..28801, 28901..29001, 29206..29402, 29446..29476, 29582..>29713)	/locus-tag="An14g05200"
CDS	join(28642..28681, 28733..28801, 28901..29001, 29206..29402, 29446..29476, 29582..29713)	/locus-tag="An14g05200"
		/note="unnamed protein product; Title: questionable ORF" /codon-start=1 /protein-id="CAK42081.1" /db-xref="GI:134081826" /translation="MGVNLGVVQSDAGMEVKKID TVWGGQDPRVEKGGVGGECINGRR ARSIGGGVWTPHLPTDKASWRTKKEPDKAARIT WNFPQCWPESKASTGNPACQARRS GGRGVFVAVRWMKQQSSWMDTREYYHCSSSGSR YVDDVGDVAAMFELISPVRCSSSEL LKSIIGPGTKGTYLSIIMIYSHRVDSTLI"
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intron	28682..28732	/locus-tag="An14g05200"
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exon	28733..28801	/locus-tag="An14g05200"
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intron	28802..28900	/locus-tag="An14g05200"
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exon	28901..29001	/locus-tag="An14g05200"
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intron	29403..29445	/locus-tag="An14g05200"
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exon	29446..29476	/locus-tag="An14g05200"
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intron	29477..29581	/locus-tag="An14g05200"
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exon	29582..29713	/locus-tag="An14g05200"
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mRNA	join(<30773..30823, 30902..>31030)	/locus-tag="An14g05210"
CDS	join(30773..30823, 30902..31030)	/locus-tag="An14g05210"
		/note="unnamed protein product; Title: weak similarity to protein fragment SEQ ID NO:24290 from patent EP1033405-A2 - Arabidopsis thaliana"
		/codon-start=1
		/protein-id="CAK42082.1"
		/db-xref="GI:134081827"
		/translation="MLPMDVDIHPPVCMSMQLVS YQLGPKVTKMVSNAFRLFASRVGF TTHPIPSLESPSTPF"
exon	30773..30823	/locus-tag="An14g05210"
		/number=1
intron	30824..30901	/locus-tag="An14g05210"
		/number=1
exon	30902..31030	/locus-tag="An14g05210"
		/number=2
gene	complement(<32776..>347	/locus-tag="An14g05220"
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mRNA	complement(join(<32776..	/locus-tag="An14g05220"
	.32888,32979..33084, 33161..33253, 33402..33450, 33632..33776, 33997..34090, 34194..34227, 34305..>34762))	
CDS	complement(join(32776..	/locus-tag="An14g05220"
	32888,32979..33084, 33161..33253, 33402..33450, 33632..33776, 33997..34090, 34194..34227, 34305..34762))	
		/note="unnamed protein product; Title: weak similarity to furin-like protein 1 Furl - Drosophila melanogaster"
		/citation=[14]
		/codon-start=1

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                                STQSRGQSGMLGLHTRMRQGGEQANVSKSRKSKS
                                ISKSTGVPQNGNPEYFWKCAAEAE
                                WNAHDQLKGTQYFLDFHPKRRTAATGAGGSCPA
                                HESYRIGKRRSPSQKGKLLLLIYS
                                VPKRTIAGAVETIQSSTAVRSFIGGQVQRKPSL
                                TTEVWAHRQQQQQQQPQDEAIQDG
                                QINSVLVMACDGWCPSLGRSGHGIGVLVMILNSY
                                FVWDDQCQFADFHTASCSLARLTS
                                SRGTYAKKSRIGSFVQIHPNEPSSTKYTV"
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intron    complement(32889..32978 /locus-tag="An14g05220"
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exon      complement(32979..33084 /locus-tag="An14g05220"
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intron    complement(33254..33401 /locus-tag="An14g05220"
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)
                                /number=5
intron    complement(33777..33996 /locus-tag="An14g05220"
)
                                /number=5
exon      complement(33997..34090 /locus-tag="An14g05220"
)
                                /number=6
intron    complement(34091..34193 /locus-tag="An14g05220"
)
                                /number=6
exon      complement(34194..34227 /locus-tag="An14g05220"
)
                                /number=7
intron    complement(34228..34304 /locus-tag="An14g05220"
)
                                /number=7
exon      complement(34305..34762 /locus-tag="An14g05220"
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gene      <35094..>35591 /locus-tag="An14g05230"
mRNA      join(<35094..35340, /locus-tag="An14g05230"

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35443..35474,
35526..>35591)
CDS      join(35094..35340,      /locus-tag="An14g05230"
35443..35474,
35526..35591)

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TGNGSRSTDREIRCTPRSGCSRRM
PGYGSVCTGFPVWQLELPWSGIHDPATGLSEQSG
NNFPGEVCGEGERGQGR LQKSKGC
IIDMTARSPCAL"

exon      35094..35340      /locus-tag="An14g05230"
                                     /number=1
intron    35341..35442      /locus-tag="An14g05230"
                                     /number=1
exon      35443..35474      /locus-tag="An14g05230"
                                     /number=2
intron    35475..35525      /locus-tag="An14g05230"
                                     /number=2
exon      35526..35591      /locus-tag="An14g05230"
                                     /number=3
gene      complement(<35692..>374 /locus-tag="An14g05240"
65)
mRNA      complement(join(<35692. /locus-tag="An14g05240"
.35854,36343..36411,
36584..36607,
36775..36906,
36960..36967,
37367..>37465))
CDS      complement(join(35692.. /locus-tag="An14g05240"
35854,36343..36411,
36584..36607,
36775..36906,
36960..36967,
37367..37465))

/note="unnamed protein product;
Title: questionable ORF"
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/protein-id="CAK42085.1"
/db-xref="GI:134081830"
/translation="MPNHRPARRNKRFLNIYHPP
IQPSIPIIHQDLEVKQTNGLT YLT
TYWIAIYPSRVMDV IIVISVMFVDDGDVRLYDK
AIVGYMADGRKHEDYSHSHYILSA
LG GGFATPRTPARVGRLLYEPKRSVAAWNNGAHA
DIERYRKPD SRGQMDMREKDN YGV DNSK"

exon      complement(35692..35854 /locus-tag="An14g05240"
)
                                     /number=1
intron    complement(35855..36342 /locus-tag="An14g05240"
)
                                     /number=1
exon      complement(36343..36411 /locus-tag="An14g05240"
)
                                     /number=2
intron    complement(36412..36583 /locus-tag="An14g05240"
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exon      complement(36584..36607 /locus-tag="An14g05240"

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/number=3
intron complement(36608..36774 /locus-tag="An14g05240"
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/number=3
exon complement(36775..36906 /locus-tag="An14g05240"
)
/number=4
intron complement(36907..36959 /locus-tag="An14g05240"
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exon complement(36960..36967 /locus-tag="An14g05240"
)
/number=5
intron complement(36968..37366 /locus-tag="An14g05240"
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/number=5
exon complement(37367..37465 /locus-tag="An14g05240"
)
/number=6
gene <40106..>40899 /locus-tag="An14g05250"
mRNA join(<40106..40139, /locus-tag="An14g05250"
40184..>40899)
CDS join(40106..40139, /locus-tag="An14g05250"
40184..40899)
/EC-number="1.-.-.-"
/inference="profile:COGS:COG1028"
/inference="profile:PFAM:PF00106"
/note="unnamed protein product;
Function: it is suggested that the
ORFL15 protein of S. spinosa is
involved in oxido-reduction during
spinosyn biosynthesis. Remark:
Spinosyns are insecticidal
microlides which are useful for
the control of arachnids,
nematodes and insects. Similarity:
SDR is a very large family of
enzymes, most of which are known to
be NAD- or NADP-dependent
oxidoreductases with different
specificities. Similarity: the
predicted ORF shows strong
similarity to several hypothetical
and described members of the short
chain dehydrogenase (SDR) protein
family. Title: strong similarity
to protein involved in spinosyn
biosynthesis ORFL15 from patent
W09946387-A1 -Saccharopolyspora
spinosa"
/codon-start=1
/protein-id="CAK42086.1"
/db-xref="GI:134081831"
/db-xref="GOA:A2R3R8"
/translation="MAAEQKLVLITGANQGIGFE
TAKNLILSDNYHVILGSRDPAKGE
EAAKTLEAVPGIKGSVSSIQIDVTDDQSVDNAAA
QIKAQYGRDLILVNNAAMSSMKHP
PSREAMRQILDVNVVGALSTTEAFLDLLRNSSEK
RLVFVSSSTGSIIRAADPSSPFHI
ASATEYRASKAALNMMMVLYMCRLKDEGFKVFGA

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exon	40106..40139	DPGLCATNLTGDPESLRRRNAAEP SDGGERVATVVKGERDADVGVKLVGVGVSPF"
intron	40140..40183	/locus-tag="An14g05250" /number=1
exon	40184..40899	/locus-tag="An14g05250" /number=2
gene	<41237..>43709	/locus-tag="An14g05260"
mRNA	join(<41237..41527, 41586..41762, 41850..43150, 43289..>43709)	/locus-tag="An14g05260"
CDS	join(41237..41527, 41586..41762, 41850..43150, 43289..43709)	/locus-tag="An14g05260"

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 /inference="profile:PFAM:PF01406"  
 /inference="similar to AA  
 sequence:PIR:S63220"  
 /note="unnamed protein product;  
 Catalytic activity: ATP +  
 L-cysteine + tRNA(cys) = AMP +  
 pyrophosphate +  
 L-cysteinyl-tRNA(cys). Similarity:  
 YNL247W of *S. cerevisiae* belongs  
 to class-I aminoacyl-tRNA  
 synthetase family. Title: strong  
 similarity to cysteine--tRNA  
 ligase YNL247w - *Saccharomyces  
 cerevisiae*"  
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 PPLKVWNSLTRSKTPFVPLDPKGR  
 KVKWYACGPTVYDDAHLGHARNYVSTDILRRILR  
 DYFKFDVEFVMNITDVDDKIILRG  
 RQQHLFNKYIAEHPTVTPDVLETARKAYSAYIKK  
 NLPLVDPDTEPENFVAEAQKTVTA  
 TTSAIAEAAQKLAGIDAASSKAFYDAAQDVFCFY  
 LDVTEGSTIPGDAHEIFTKLTKKY  
 EDHFMRDMRDLNVLDPAVTRVTEYGQQIADFVE  
 KIVANKFGYVTS DGSVYFDIKA FE  
 EAGNHYARLEPWNRNNQPLLRDGEGLSRATEKK  
 SSDDFALWKASRPGEPSWSSKWGQ  
 GRPGWHIECSAMASSCLGSQIDIHSGGIDLAFPH  
 HDNELAQSEAYWCEHKQQWVNYFL  
 HMGHLSIQGSKMSKSLKNFTTVKDALERG DYTPR  
 SLRIVFLLGGWRDGEITDDL IKN  
 ASSWEEKLNNFFVKAKDPSSFRSSDEAPTSSSET  
 LSQALKSTQEKVHEYFCDSFDTPK  
 VMAAISELVTTFNALDSQTLDLKVVESMGTWVTQ  
 IVTIFGLNGAASSDSCGIGWEGTD  
 IPEAAKRFLYPLSAMRDTLRQAAILDDTKQASKD  
 ILSLCDRLRNVDLFLNLGIYLEDRE

		NKPALVRPVTKDMLQAREEQARKALLKQQEKEKQ EKLAQERLEKGKLNPNVEMFRTSEY SAWDEDGIPTKDAAGEPLAKSKSKKLKRDWERQK KAHEAWLASQNGK"
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intron	41528..41585	/locus-tag="An14g05260" /number=1
exon	41586..41762	/locus-tag="An14g05260" /number=2
intron	41763..41849	/locus-tag="An14g05260" /number=2
exon	41850..43150	/locus-tag="An14g05260" /number=3
intron	43151..43288	/locus-tag="An14g05260" /number=3
exon	43289..43709	/locus-tag="An14g05260" /number=4
gene	<43954..>45254	/locus-tag="An14g05270"
mRNA	join(<43954..43984, 44194..44823, 44878..45059, 45108..>45254)	/locus-tag="An14g05270"
CDS	join(43954..43984, 44194..44823, 44878..45059, 45108..45254)	/locus-tag="An14g05270"  /codon-start=1 /product="hypothetical protein" /protein-id="CAK42088.1" /db-xref="GI:134081833" /translation="MALDNARRVYIQLNNIDLHT ITTDLSRLHVQRLMRLTAKQASDI RELSICSASGGPLSLGYRVLPSCPLKSQASKDLR EALKKKLKQCRTLRI SAVEIKHTDY ELAWMGAIDMTHSVLSAFCETQNSLKS LTLD FRT DNVASLLRGGLERIPSYGPAELSR FPFGSSRINHISLNLNANIAGSPGLCERLLHPLY TRYGVNEVSLDLGKAYAENVVLDV LRGMGHRMLEPKLKQYCHSLRVLT MENIIFRYNY WLRFLHSLKREFRRLQEVNLFWEV NTSSESTSLITQWNHNTIYDNTQTRVTYTGP EEH GALTAEKIAS EDPLSVHL"
exon	43954..43984	/locus-tag="An14g05270" /number=1
intron	43985..44193	/locus-tag="An14g05270" /number=1
exon	44194..44823	/locus-tag="An14g05270" /number=2
intron	44824..44877	/locus-tag="An14g05270" /number=2
exon	44878..45059	/locus-tag="An14g05270" /number=3
intron	45060..45107	/locus-tag="An14g05270" /number=3
exon	45108..45254	/locus-tag="An14g05270" /number=4
gene	<46541..>47683	/locus-tag="An14g05280"
mRNA	join(<46541..47034, 47092..47344, 47501..>47683)	/locus-tag="An14g05280"
CDS	join(46541..47034,	/locus-tag="An14g05280"

47092..47344,  
47501..47683)

exon	46541..47034	/locus-tag="An14g05280"
intron	47035..47091	/number=1
exon	47092..47344	/locus-tag="An14g05280"
intron	47345..47500	/number=2
exon	47501..47683	/locus-tag="An14g05280"
gene	<48251..>50618	/number=3
mRNA	join(<48251..48422, 48475..>50618)	/locus-tag="An14g05290"
CDS	join(48251..48422, 48475..50618)	/locus-tag="An14g05290"

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RDKKMHAFFHLSQEAKRQRLQDK  
ILATHAGIEEYSAGYLKPWQLLKLKIDASEVNIS  
SKDIIKFRPCFFSPLPTDTIRTCL  
SKQPNKKSPDENS LGYAGRAMPCPSTVALMHYPL  
ILDLFREKYATSVRKGFCLDSLTT  
LRECGATSKGKWKQPGLELAEKLSTERWQILRI  
LEDLEHEVPHAVCDIRQNIQVDRK  
KGLTVAEVKAIMRVMAVRIGLDCYRPHFLMPTLM  
DLNITLSSSSFATTAASQSERPPI  
SRRIHRQDRARELAPLTPHGGKEGHHFQSRRI"  
/inference="profile:PFAM:PF03169"  
/inference="similar to AA  
sequence:UniProtKB:SPBC29B5.2"  
/note="unnamed protein product;  
Function: isp4 of S. pombe is a  
membrane oligopeptide transporter.  
Remark: isp4 of S. pombe was  
originally identified by  
subtractive screening as gene  
induced during the sexual  
differentiation process.  
Similarity: the predicted A. niger  
protein shows strong similarity to  
protein isp4 of S. pombe, which  
belongs to the OPT subfamily of  
transporters specific for small  
oligopeptides (from the C.  
albicans OPT1 gene). Title: strong  
similarity to protein isp4p  
-Schizosaccharomyces pombe plasma  
membrane"  
/citation=[20]  
/citation=[52]  
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VLGFIFTIVGSGINQFFSLRYPSV"

		HIVSLVAELLAYPCGVFLAKVLPLWTISLGRGLGS FTLNPDRHFNIKEHALIVIMSNVS FGYGSADSTNIIQASSARFYNFGLSAGFSVLVVL CAQLLGFGVAGLAAPWLVEPARII WPQVLSNCAMLETLHSRANTVANGWKISRLRFFL YVTAGGFVWYFFPGLMFTALSYFT WICWIAPRNVVVNQLFGMQTGLGLSPITFDWSQV AYNTNPLLSPSWAAINVFAGFALF FWIVVPGIYYSNTWFTAYLPLMTADVYDRTGTVY DTARVISADNTLDVDAYRQYSPPY LPATYAFVYGLSFASITAVLTHIGVWHGKEVWAA LKGKNKLDIHARLMKSYKKTPWYW YAAIIAIIITAIAIVMVEVYHTKLPVYGVLGLII PAIYMVPCGIIQGITNVDANQLNV LAEFIGGYMFEGKPLANMIFKILSTDVVGQGVYF AMDMKLGHYLKIPRTLFMQAQGLA TILGALTQAGVTIWMLGHIQDICSSDQSDGFTCP NGRTVYSSSVIWGLVGPRRLYSVG RIYSSLLHFFWIGAIAPLITYFLYKYTRKQFWKY INWPLIFVGTYNVPPATGINYSSW ALVNFAFNHFIKKRFFAWKKYNYILAAALDTGL ALSGIVIFFCISYPGAVFPDWWGN TVYVNTADGEGVAYKSMPEVGYFGPANGTWS"
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intron	48423..48474	/locus-tag="An14g05290"
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exon	48475..50618	/locus-tag="An14g05290"
		/number=2
gene	complement(<51277..>53277)	/locus-tag="An14g05300"
mRNA	complement(join(<51277..51279,51332..51599,51656..51726,51783..51947,52973..53002,53059..>53277))	/locus-tag="An14g05300"
CDS	complement(join(51277..51279,51332..51599,51656..51726,51783..51947,52973..53002,53059..53277))	/inference="profile:COGS:COG0724" /inference="profile:PFAM:PF00076" /inference="similar to AA sequence:SWISSPROT:YRA1.YEAST" /note="unnamed protein product; Complex: YRA1 of S. cerevisiae mediates nuclear export of mRNA by interacting with several other protein factors, like Mex67. Function: YRA1 of S. cerevisiae is an mRNA-binding protein involved in the nuclear export of mRNA towards the cytoplasm. Remark: although the gene structure looks strange,the strong similarity to known proteins justify the model. Similarity: YRA1 S. cerevisiae belongs to the evolutionarily conserved REF (RNA and export

factor binding proteins) family of  
hnRNP-like proteins. Title: strong  
similarity to RNA annealing  
protein Yra1 - Saccharomyces  
cerevisiae nucleus"

/citation=[36]

/citation=[67]

/citation=[68]

/citation=[86]

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/protein-id="CAK42091.1"

/db-xref="GI:134081836"

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TTKAAKAPGKAVQNGHPVSTESKIMVSGLPSDVN

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MKIEVVVDASHAPEVSAPKPLGER

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intron complement(51600..51655 /locus-tag="An14g05300"

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intron complement(51948..52972 /locus-tag="An14g05300"

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/number=4

exon complement(52973..53002 /locus-tag="An14g05300"

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/number=5

intron complement(53003..53058 /locus-tag="An14g05300"

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/number=5

exon complement(53059..53277 /locus-tag="An14g05300"

)

/number=6

gene complement(<54264..>550 /locus-tag="An14g05310"

12)

mRNA complement(join(<54264. /locus-tag="An14g05310"

.54902,54965..>55012))

CDS complement(join(54264.. /locus-tag="An14g05310"

54902,54965..55012))

/inference="profile:COGS:COG5491"

/inference="profile:PFAM:PF03357"

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/feature=1
/note="unnamed protein product;
Function: the S. cerevisiae
homolog Did3p is a class E Vps
factor, which function in the
maturation of a late
endosome/prevacuolar compartment
into multivesicular bodies that
then fuse with the vacuole.
Remark: DID3 of S. cerevisiae is
also called YKL041w. Remark: S.
cerevisiae Did3p is probably
involved in the ubiquitin-mediated
maturation of multivesicular
bodies. Title: strong similarity
to protein involved in vacuolar
protein sorting Did3 -
Saccharomyces cerevisiae endosome"
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/citation=[76]
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NQLIRVNTNRQLDRDIAQLKTLESK
TRQYIMNSSKRAQRNPSQAKQANMEAKTFARELV
RIRKQSTRLHTSRAQLQSVQMQRVN
EAFSVRKIQGSLKKSTGIMKDVNTLVQMPELNAT
MRQLSTELVRAGIIEEMVDDAIPN
NELLEEEEEEEAEEVEVDKVLQEILHGKLSQVEGVQ
PEKPLEEAPEPEDEFADQEATLEQ
MRGRLEALKS"
exon complement(54264..54902 /locus-tag="An14g05310"
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intron complement(54903..54964 /locus-tag="An14g05310"
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exon complement(54965..55012 /locus-tag="An14g05310"
)
/number=2
gene <55690..>56601 /locus-tag="An14g05320"
mRNA join(<55690..55720, /locus-tag="An14g05320"
55913..56238,
56300..56464,
56527..>56601)
CDS join(55690..55720, /locus-tag="An14g05320"
55913..56238,
56300..56464,
56527..56601)
/inference="similar to AA
sequence:PIR:T39220"
/note="unnamed protein product;
Function: WOS2 of S. pombe is a
cochaperone protein that interacts
with cdc2 in the control of the
M-G1 transition. Similarity: WOS2
of S. pombe belongs to the p23 /
wos2 family. Title: strong
similarity to cell cycle regulator
p21 protein wos2p -
Schizosaccharomyces pombe"
/citation=[65]

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exon	55690..55720	/locus-tag="An14g05320"
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intron	55721..55912	/locus-tag="An14g05320"
		/number=1
exon	55913..56238	/locus-tag="An14g05320"
		/number=2
intron	56239..56299	/locus-tag="An14g05320"
		/number=2
exon	56300..56464	/locus-tag="An14g05320"
		/number=3
intron	56465..56526	/locus-tag="An14g05320"
		/number=3
exon	56527..56601	/locus-tag="An14g05320"
		/number=4
gene	<57642..>58927	/locus-tag="An14g05330"
mRNA	join(<57642..57701, 57764..57781, 57888..58214, 58242..58438, 58498..>58927)	/locus-tag="An14g05330"
CDS	join(57642..57701, 57764..57781, 57888..58214, 58242..58438, 58498..58927)	/locus-tag="An14g05330"
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exon	57642..57701	/locus-tag="An14g05330"
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intron	57702..57763	/locus-tag="An14g05330"
exon	57764..57781	/number=1
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intron	57782..57887	/locus-tag="An14g05330"
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exon	57888..58214	/locus-tag="An14g05330"
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intron	58215..58241	/locus-tag="An14g05330"
		/number=3
exon	58242..58438	/locus-tag="An14g05330"
		/number=4
intron	58439..58497	/locus-tag="An14g05330"
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exon	58498..58927	/locus-tag="An14g05330"
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gene	<59882..>61522	/locus-tag="An14g05340"
mRNA	join(<59882..60273, 60344..60429, 60510..61189, 61367..61434, 61480..>61522)	/locus-tag="An14g05340"
CDS	join(59882..60273, 60344..60429, 60510..61189, 61367..61434, 61480..61522)	/locus-tag="An14g05340"
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		/inference="similar to AA
		sequence:PIR:E83710"
		/note="unnamed protein product;
		Title: strong similarity to
		hypothetical protein BH0485 -
		Bacillus halodurans"
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		/protein-id="CAK42095.1"
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		LKDYYDADSCGQVDWHSYTLQGAE
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		NETYKQALDTLHDAFNARTRDSEG
		AFWYFNPYPNWGVLEGLYPLGSFISMWKTYFEPT
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		GNYIESSGSAQFVYGLLKGARLGY
		LQGKTPNGVGYTDAADKCYNILVSEFVKEEADGS
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intron	61435..61479	/number=4 /locus-tag="An14g05340"
exon	61480..61522	/number=4 /locus-tag="An14g05340"
gene	complement(<62253..>63796)	/number=5 /locus-tag="An14g05350"
mRNA	complement(join(<62253..62358,62418..62491,62545..62677,62734..63473,63541..63615,63704..>63796))	/locus-tag="An14g05350"
CDS	complement(join(62253..62358,62418..62491,62545..62677,62734..63473,63541..63615,63704..63796))	/locus-tag="An14g05350"

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 Function: ayg1 of A. fumigatus has  
 an unknown function, but it is  
 contained in the gene cluster  
 responsible for conidial  
 pigmentation. Phenotype: ayg1 null  
 mutants of A. fumigatus have  
 yellowish-green conidia. Title:  
 strong similarity to hypothetical  
 yellowish-green 1 ayg1 -  
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CDS	join(63948..64102, 64223..64301, 64493..64828, 64917..65270)	/locus-tag="An14g05360"
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mRNA	join(<65395..65730, 65792..66891, 66909..>67116)	/locus-tag="An14g05370"
CDS	join(65395..65730, 65792..66891, 66909..67116)	/locus-tag="An14g05370"

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 Similarity: the predicted ORF  
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 cluster; abr1 mutants have brown  
 conidia, and the proposed function  
 of abr1 is multicopper oxidase.  
 Title: strong similarity to cell  
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 - Saccharomyces cerevisiae plasma  
 membrane"  
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exon	66909..67116	/locus-tag="An14g05370" /number=3
gene	complement(<67552..>687 35)	/locus-tag="An14g05380"
mRNA	complement(join(<67552.. .67985,68039..>68735))	/locus-tag="An14g05380"
CDS	complement(join(67552.. 67985,68039..68735))	/locus-tag="An14g05380"  /EC-number="1.4.3.3" /inference="profile:COGS:COG0665" /inference="profile:PFAM:PF01266" /note="unnamed protein product; Catalytic activity: the D-amino acid oxidase catalyzes the reaction: D-Amino acid + H2O + O2 = 2-Oxo acid + NH3 + H2O2. Catalytic activity: the D-amino acid oxidase has a wide specificity for D-amino acids, acting also on glycine. Cofactor: D-amino acid oxidase is a flavoprotein (FAD is the cofactor). Title: strong similarity to D-amino acid oxidase DAO1 - Trigonopsis variabilis" /citation=[47] /codon-start=1 /protein-id="CAK42099.1" /db-xref="GI:134081844" /db-xref="GOA:A2R3T1" /translation="MAEKETIVVIGYVVSQCHPL NHNNSTTNHPHPFQPNRAGIIGLT TALYIQQRLSPSQRVLIAARDFPHSTSLNYASPW AGAHYRPVPGSNAQHTREETQARR TYAHFKTLAAQEPGAGVQSTTGIEYLENPPAEYL NEKNIQAAYGHLDFEYLQPGQMP GDVKWAVKYKTFVNVSPVYCAWLLREFVLRGGEV KEYTFVDLREGFYLAERVRAVVNC SGLGFGDEKSYIIRGQTCLVRNPCSATITRQNSD GSWSFCIPRPLGGGTIIIGGTKQPH NWDPNPSMETRAQLLANAAKWFPFEEGSKEEFDV IRDIVGRRPAREGGMRIEVEKINQ GQEVIVHAYGAGGRGFELSWGVAEDVYDLMRQNG LIKAKASL"
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Title: strong similarity to
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/note="unnamed protein product;
Title: weak similarity to

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gene	<73435..>78401	/locus-tag="An14g05410"
mRNA	join(<73435..73846, 73906..74029, 74087..74398, 74453..75231, 75292..>78401)	/locus-tag="An14g05410"
CDS	join(73435..73846, 73906..74029, 74087..74398, 74453..75231, 75292..78401)	/locus-tag="An14g05410"  /inference="similar to AA sequence:UniProtKB:NCB1K11.22" /note="unnamed protein product; Similarity: A. niger EST EMBLEST:BE760323 corresponds to the 3' portion of the last exon and a fragment of the putative 3'-UTR of the gene. Title: strong similarity to hypothetical protein CAD21189.1 - Neurospora crassa" /codon-start=1 /protein-id="CAK42102.1" /db-xref="GI:134081847" /translation="MVELSWNRNPVQVPDPRPSR MKPAAPPVSTQPQTTPARLEPCAS TASLLLYAQGSVIVCLHHDTLALERRFENHQDDI GFIYVDNVSERGAGRLVVSVDVSQ TAIVWDLFTGSLARFASFEQLKVAAMRNGNVA FGNEKGDVIIFEPSTSEHISCRTI FDPITALAPATDCRTYAIGYQNGSIMLATLHPTF SILHTMSTSRGPSAIIISLAWHASS SKQKSDMLATLAANGDLRVWSVAKPPQKEAPRVI RVLKRS DGSPATEPKWMAWSKNGR IVQFLEGETWAWDVRTKHVTYEPITIDNPRGFA NYGPTATLFTLGPQYTVQQYDIDS PAMVANVQHAPSGALPAPMEQPRRLRTLQEPPTMR ESGAMFGSRRTPFDTNGIEAVRQQ RADVASPVNRSHANSVTNSVSSKASSGMHKIPFS PPSRSGQTTTSFSLTSASGRETPQ PSGASYAYASSVMSSTKSSRAGSRLRNEVQLSP AEKPVDLFPFTRARLNDVPYGHQ PLDESRLTPDDL RQQMLSVVFGFDGDIEELIRDE LSNHPEASQSAVLLAQWIGESDTD

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/note="unnamed protein product;  
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with different specificities.
Similarity: the predicted ORF
shows strong similarity to several
hypothetical and described members
of the short chain dehydrogenase
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similarity to meso-2,3-butanediol
dehydrogenase (D-acetoin forming)
budC - Klebsiella pneumoniae"
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CDS	complement(join(87776..88536,88589..89339))	/locus-tag="An14g05470"
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and phosphorylated sphingoid base  
levels, and modulates stress  
responses through sphingolipid  
metabolites. Remark: YSR3 of *S.*  
*cerevisiae* is also called YKR053c.  
Similarity: *A. niger* EST  
EMBLEST:BE760128 comprises part of  
the putative 5'-UTR of the gene  
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Remark: RHO1 gene encodes a
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of its recently identified

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CDS	complement(join(119272. .119830,119883..120299, 120386..120822, 120879..121016, 121097..121189))	/EC-number="6.2.1.12" /inference="profile:COGS:COG0318" /inference="profile:PFAM:PF00501" /note="unnamed protein product; Catalytic activity: ATP + 4-coumarate + CoA = AMP + pyrophosphate + 4-coumaroyl-CoA. Pathway: flavonoids, stilbene and lignin biosynthesis. Remark: the phenylpropanoid enzyme 4-coumarate:coenzyme A ligase (4CL) plays a key role in general phenylpropanoid metabolism. 4CL is related to a larger class of prokaryotic and eukaryotic adenylate-forming enzymes and shares several conserved peptide motifs with these enzymes. Similarity: belongs to the Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II. Title: strong similarity to 4-coumarate-CoA ligase 3 4CL3 - Populus balsamifera" /citation=[83] /codon-start=1 /protein-id="CAK42124.1" /db-xref="GI:134081869" /db-xref="GOA:A2R3V6" /translation="MIFEPAARAPVPCTDVISYV FSDPPYDHDEPIYVDVHNPSRSIS YNQARTIVRQLVSGLRAGVQKGDCVAIHSFNDI YYTMLVLAIVGAGGIFTGSNPAYT AFELGHHFRSSATNFVITEPEHLDAITTAKAAS IPEHRIRVFDVLGQSVPDGAVSWT

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		and causes black spot of Japanese
		pear. Transformation of the wild
		type with AKTR-1- and
		AKT3-1-targeting vectors produced
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intron	131324..131387	/number=1 /locus-tag="An14g05680"
exon	131388..131502	/number=1 /locus-tag="An14g05680"
intron	131503..131554	/number=2 /locus-tag="An14g05680"
exon	131555..131602	/number=2 /locus-tag="An14g05680"
intron	131603..131644	/number=3 /locus-tag="An14g05680"
exon	131645..131662	/number=3 /locus-tag="An14g05680"
gene	<134201..>135346	/number=4 /locus-tag="An14g05690"
mRNA	join(<134201..134238, 134452..134502, 134768..134993, 135113..>135346)	/locus-tag="An14g05690"
CDS	join(134201..134238, 134452..134502, 134768..134993, 135113..135346)	/locus-tag="An14g05690"
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exon	134201..134238	/locus-tag="An14g05690"
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exon	134452..134502	/number=1 /locus-tag="An14g05690"

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intron	134503..134767	/locus-tag="An14g05690"
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intron	134994..135112	/locus-tag="An14g05690"
		/number=3
exon	135113..135346	/locus-tag="An14g05690"
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mRNA	6476) complement(join(<135466	/locus-tag="An14g05700"
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	135676..135753,	
	136059..136189,	
	136290..136364,	
	136405..>136476))	
CDS	complement(join(135466.	/locus-tag="An14g05700"
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	136059..136189,	
	136290..136364,	
	136405..136476))	
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		/translation="MPMKDSRQLTCRLNSWIRLQ LEYRAGIYYSDLTRKKPIVPSGT KPRCNRYLVQHYLYGIKRSCPARNSGSKCSGCTD AHDFMDARMENAKELQKVLDSGPS RIEGSWIIPDIHTSAMSATEDDSGVMGTGLGVLSG CTLAFAKDRANWNDDDGIPG"
exon	complement(135466..1355	/locus-tag="An14g05700"
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intron	complement(136190..1362	/locus-tag="An14g05700"
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exon	complement(136290..1363	/locus-tag="An14g05700"
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		/number=4
exon	complement(136405..1364	/locus-tag="An14g05700"
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138078..138298,
138437..>138530))
CDS       complement(join(137703. /locus-tag="An14g05710"
.137767,137825..137999,
138078..138298,
138437..138530))

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/note="unnamed protein product;
Similarity: although the
similarity to Rhp16 of S. pombe is
weak, some motifs in the predicted
ORF suggest that it might be
involved in DNA binding and
repair. Title: weak similarity to
RAD16 nucleotide excision repair
protein homolog rhp16p -
Schizosaccharomyces pombe"
/citation=[32]
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LVDHATYEPDKPTLIICPPHLVWQWASEIKKFTS
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exon      complement(138078..1382 /locus-tag="An14g05710"
98)
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139649..139772,
139813..139963,
140010..140120,
140192..140244,

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intron	139253..139342	/number=1 /locus-tag="An14g05720"
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intron	139428..139648	/number=2 /locus-tag="An14g05720"
exon	139649..139772	/number=2 /locus-tag="An14g05720"
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gene	complement(<140647..>14 2006)	/number=7 /locus-tag="An14g05730"
mRNA	complement(join(<140647 ..141004, 141055..141527, 141590..141657, 141707..141743, 141796..141815, 141865..141876, 141952..>142006))	/locus-tag="An14g05730"
CDS	complement(join(140647. .141004,141055..141527, 141590..141657, 141707..141743,	/locus-tag="An14g05730"



141796..141815,  
 141865..141876,  
 141952..142006))

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sequence:UniProtKB:AF119672.1"
/note="unnamed protein product;
Function: PTH11 of M. grisea is
required for appressorium
differentiation in response to
inductive surface cues. Function:
as do most fungal plant pathogens,
M. grisea differentiates an
infection structure specialized
for host penetration called the
appressorium. Phenotype: M. grisea
cells null mutant for PTH11 are no
more pathogenic. Similarity: the
length of the predicted ORF is
only one half of the M. grisea
PTH11. Title: similarity to
integral membrane protein PTH11 -
Magnaporthe grisea"
/citation=[63]
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FVKIALLSILIRIFNPYRSKIYFI
YGLLGCLCIYYIVAEIVKIRMCDPVPAYWTQDPK
ARCLNQRAALIADSVISVVTDFII
LILPLPLTWSLQMSRNKKLRVIGMLSAGGLATAF
SLYRLVLVLRDGSSRDQTIVFMIV
ILSGNAEGGVAMICACLPTVNILINKLRKKEYSS
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exon complement(141055..1415  
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intron complement(141528..1415  
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exon complement(141590..1416  
57)

intron complement(141658..1417  
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exon complement(141707..1417  
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exon	complement(141952..142006)	/locus-tag="An14g05730"	
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mRNA	complement(join(<142716..142868, 142941..143171, 143244..143322, 143423..143759, 143845..>143896))	/locus-tag="An14g05740"	
CDS	complement(join(142716..142868, 142941..143171, 143244..143322, 143423..143759, 143845..143896))	/locus-tag="An14g05740"	
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exon	complement(143845..143896)	/number=4 /locus-tag="An14g05740"
gene	<143978..>145355	/number=5 /locus-tag="An14g05750"
mRNA	join(<143978..144235, 144298..144933, 144984..>145355)	/locus-tag="An14g05750"
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		/EC-number="1.3.1.42" /inference="profile:COGS:COG1902" /inference="profile:PFAM:PF00724" /inference="similar to AA sequence:UniProtKB:AF293653.1" /note="unnamed protein product; Catalytic activity: OPR3 of A. thaliana catalyzes the reaction: 8-[(1R,2R)-3-Oxo-2-{(Z)-pent-2-enyl}cyclopentyl]octanoate + NADP+ = (15Z)-12-Oxophyto-10,15-dienoate + NADPH. Phenotype: A. thaliana ORP3 null mutants are male-sterile due to defects in pollen release caused by a delay in the stomium degeneration program. Remark: Jasmonic acid (JA) and its precursor 12-oxophytodienoic acid (OPDA) act as plant growth regulators and mediate responses to environmental cues. Title: strong similarity to 12-oxo-phytodienoate reductase OPR3 - Arabidopsis thaliana" /citation=[71] /citation=[75] /codon-start=1 /protein-id="CAK42136.1" /db-xref="GI:134081881" /db-xref="GOA:A2R3W8" /translation="MTIVQAQGADSKLFQPLAIA NGKLTLSHRVVHAPLTRNRGEPLN SNSTPENPNRIWYPGDLVVEYYRQRATPGGLIIS EGIPPSLESNGMPGVSGLFTEEQA AGWKRVDTVHAQGGYIYQQLWHAGRATVPQMTG YPPVSASASVWDDPEERYTHPAVG DSEPVRYSDHPPIELTVAHIKQTIQDYCKAAKTA MDIGFDGVELHSGNGYLPEQFLSS NINRRTDDYGGTPEKRCRFVLELMDELAQTVGQE NLAIRLTPFGLYNQARGEQRVETW TYLCESLQAHPHLSYVSFVEPRYEQIHSYEEKD AFLRSWGLSSVDLSSFRKIFGSTP FFSAGGWDQTNWGVLEAGKYDALLYGRYFTSNP DLVERLRKGIPFAPYDRTRFYGP EDSAFHYVDYEPAPQNSTGQESVNVSVRL"
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exon	144984..145355	/number=2 /locus-tag="An14g05750"
gene	complement(<145510..>146577)	/number=3 /locus-tag="An14g05760"
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CDS	complement(join(145510..145699,145751..145803, 145854..145876, 145933..146045, 146099..146459, 146529..146577))	/locus-tag="An14g05760"
		/EC-number="1.1.1.245" /inference="profile:COGS:COG1028" /inference="profile:PFAM:PF00106" /note="unnamed protein product; Catalytic activity: chnA of Acinetobacter catalyzes the reaction: Cyclohexanol + NAD+ <=> Cyclohexanone + NADH. Similarity: the gene model structure is confirmed by A. niger EST EMBLEST:BE759160, which covers exons 1 to 3. Title: strong similarity to cyclohexanol dehydrogenase chnA - Acinetobacter sp" /citation=[72] /codon-start=1 /protein-id="CAK42137.1" /db-xref="GI:134081882" /db-xref="GOA:A2R3W9" /translation="MACKVSGTAFITGGGNGIGK TTAFALAQNGIEAVSLLDVNESLL QRTKDELATSHPQVAVELTVGDVSKEACVDEAVR RTVERFGRIDISVHCAGIVGQPSA THELTAAEWQRVIDINQTVLLCQKAVIRQMLTQ ESRGLRLGRGTIVNVASMFGVVAP GGWSGLSAYTASKHAVVAFSKMDAKAYIQQEIRI NAICPGYTDTDMIRTYWDAGYMVP DSQRVAIGRRAQPEEIADAVLFLASPMSSYMVGS ALVVDGGYTA"
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intron	complement(145700..145750)	/number=1 /locus-tag="An14g05760"
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53)
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exon      complement(146099..146459) /number=4 /locus-tag="An14g05760"
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exon      complement(146529..146577) /number=5 /locus-tag="An14g05760"
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mRNA      complement(<147404..>147784) /locus-tag="An14g05765"
CDS       complement(147404..147784) /locus-tag="An14g05765"
exon      complement(147404..147784) /note="unnamed protein product;
Title: strong similarity to EST
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CDS       join(149275..150089, /locus-tag="An14g05780"
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/inference="similar to AA
sequence:PIR:S64014"
/note="unnamed protein product;
Function: the S. cerevisiae ERG4
gene encodes sterol C-24(28)
reductase which catalyzes the
final step in the biosynthesis of
ergosterol. Remark: ergosterol is
the precursor of vitamin D2.
Title: strong similarity to sterol

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		C-24 reductase Erg4 - Saccharomyces cerevisiae endoplasmatic reticulum" /citation=[6] /citation=[18] /citation=[22] /citation=[54] /citation=[66] /codon-start=1 /protein-id="CAK42139.1" /db-xref="GI:134081884" /db-xref="GOA:A2R3X1" /translation="MKQSKDRSPEGTSNAHEDEK PTFEFGGAPGVTMLMLGFLLMY MFIGATLYDGHLPLPDENQSI TDFLSHLVLAHT HAYPNRKAWIIYWTFLVLEGL GYL YLPGVYGKGKCLPHLNGKQLD YYCSAASSWYVTI AAALVLHFGIFRLSTLVEEFG PL MSVAICSGFLVSI IAYVSALL RGAQHRMTGSHVY DFFMGAELNPRLFQWLDKMF FEV RIPWYILFLLTLGTALKQWED YGFSGEVSFLLL AHFLYANACAKGEELIITSWD MY EKGWFMLIFWNLAGVPMSYCH CTLYLASHDPSTY KWNPIALGVLFVMIYIFAYWV WDT NSQKNLFRQAQERGKPVNRKT FPQLPWKSVKNPVC IKTKTGDSILCSGWYGMARKV HYS CDWFFAFSWGLITGFNSPFPWF YSCFFTVMIIHR ALRDIERCRCRERYGEAWREY ERRVP YLFIPVSRLELVL"
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intron	150090..150139	/locus-tag="An14g05780" /number=1
exon	150140..150471	/locus-tag="An14g05780" /number=2
intron	150472..150520	/locus-tag="An14g05780" /number=2
exon	150521..150765	/locus-tag="An14g05780" /number=3
gene	complement(<151141..>153445)	/locus-tag="An14g05790"
mRNA	complement(join(<151141..151564, 151613..151848, 151899..152339, 152378..152673, 152720..153109, 153190..153256, 153395..>153445))	/locus-tag="An14g05790"
CDS	complement(join(151141..151564,151613..151848, 151899..152339, 152378..152673, 152720..153109, 153190..153256, 153395..153445))	/inference="profile:PFAM:PF04082" /note="unnamed protein product; Similarity: the predicted protein shows similarity to several putative and described fungal transcription factors; their

common feature is the presence of a typical binuclear cluster zinc-finger, responsible for DNA binding, which is not well conserved in the predicted protein. Title: weak similarity to transcription activator prnA - *Aspergillus nidulans*"  
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RDAAYSAANTARDGQVG DYVSAALSSLKSSLD RH  
NHAMNRSGAQSPAQLNQTL LPVDL  
VVAVVKKVKSQPPFFLV SQSWLDSTRVEHLCQSI  
YFPLDPVPPGSLTLFYGILFYVIR  
DYLHAGDPDLAHFDLQLSLELCERHFVAGLSKPE  
IMFEPTLEKIQALLLGIQVLKAE  
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EQRSASIERLSSDLMTVRDKLLAIDVSRGLYADS  
LHGMAACADFIAYSVLTVIYRAQT  
HPRDVM AVSSQCYASATAALQSHLKCF TYFRGRQ  
THKQTEYVNWILLYPSFTPFVIVF  
THAITTASTADLALLQDTASSLELIKGLSRGSMH  
LYTICDAFVRAAQILVNSQQTLTG  
LEQH QDGS LVIPTTDGPGNIALPDVPWPEDTFDS  
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		/note="Function: hydrolysis of alpha-D-1,2-(4-O-methyl)glucuronosyl links in the main chain of hardwood xylans. Gene-ID: aguA"
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sig-peptide	154037..154096	
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exon	154037..156562	/gene="aguA" /locus-tag="An14g05800" /number=1
gene	<157327..>158616	/locus-tag="An14g05810"
mRNA	join(<157327..157515, 157564..>158616)	/locus-tag="An14g05810"
CDS	join(157327..157515, 157564..158616)	/locus-tag="An14g05810"  /EC-number="2.3.1.48" /inference="profile:COGS:COG5076" /inference="profile:PFAM:PF00439" /inference="similar to AA sequence:PIR:S28051" /note="unnamed protein product; Complex: GCN5 of S. cerevisiae is a component of the SAGA complex, which possesses histone acetylation function and is important for transcription in vivo. Function: GCN5 of S. cerevisiae and many other organisms acetylates histones H3 and H4 non-randomly at specific lysines, causing chromatin remodelling during transcriptional activation. Similarity: in the C-terminal part of the protein there is a bromodomain, which function may be to tether type A histone acetyltransferase to the chromatin during gene activation. Title: strong similarity to histone acetyltransferase Gcn5 - Saccharomyces cerevisiae nucleus" /citation=[21] /citation=[23] /citation=[29] /citation=[31] /citation=[34] /codon-start=1 /protein-id="CAK42142.1" /db-xref="GI:134081887" /db-xref="GOA:A2R3X4" /translation="MDGAELQSPLLDNGQPPLVA KRVTSEEPNAAADAKRLKTSDDRE APPQTNLPAATRIVPFPEKPAVVEERNCEIEFRV VNNDGSTESTVILTGLKNLFQKQL PKMTKDYIARLVYDHTLHLAICKMPLEIIGGIT FREVRHRRFAEIVFCAASSDQQVK GYGAHLMAHLKDYVRATSPVMHFLTYADNYATGY FQKQGFTKEITLDKSIWMGYIKDY EGGTLMQCSMLPRIRYLEVGRMLLKQKACVLAKL

		RPLSRNHIVHPPPPQWANGIVTLI DPLSIPAIRATGWSPDMDELARQPRHGPHFNELR RFLSKIQAHKQAWPFLSPVKNDEV PDYYNFIESPMDLSTMEERLENDTYSTPKELIND LKSIFRNCRQYNDATTIYAKSATK LEKYIYSLIKEVPEWFDLVKE"
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intron	157516..157563	/locus-tag="An14g05810" /number=1
exon	157564..158616	/locus-tag="An14g05810" /number=2
gene	<159715..>163074	/locus-tag="An14g05820"
mRNA	join(<159715..160332, 160378..160543, 160593..160722, 160785..160893, 160962..162768, 162857..>163074)	/locus-tag="An14g05820"
CDS	join(159715..160332, 160378..160543, 160593..160722, 160785..160893, 160962..162768, 162857..163074)	/locus-tag="An14g05820"

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 /inference="similar to AA  
 sequence:UniProtKB:A00968.1"  
 /note="unnamed protein product;  
 Catalytic activity: hydrolysis of  
 terminal,non-reducing  
 beta-d-galactose residues in  
 beta-d-galactosides. Function:  
 cleaves beta-linked terminal  
 galactosyl residues from  
 gangliosides, glycoproteins, and  
 glycosaminoglycans. Remark:  
 beta-galactosidase of A. niger has  
 been already patented under  
 patentnumber WO9010703 and  
 WO9716555-A1. Similarity: belongs  
 to family 35 of glycosyl  
 hydrolases. Similarity: the  
 absence of nice BLASTN  
 alignments,demonstrates that the  
 predicted ORF is just an homologue  
 of the already described  
 beta-galactosidase of A. niger.  
 Title: strong similarity to  
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 Aspergillus niger  
 extracellular/secretion proteins"  
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 LDAITPYMQAIGRIIAKAQITNGGPVILFQPENE  
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exon	162857..163074	/number=5 /locus-tag="An14g05820"
gene	complement(<163244..>165037)	/number=6 /locus-tag="An14g05830"
mRNA	complement(<163244..>165037)	/locus-tag="An14g05830"
CDS	complement(163244..165037)	/locus-tag="An14g05830"
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          166970..167082,
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CDS       complement(join(166037. /locus-tag="An14g05840"
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          sequence:UniProtKB:AF159789.1"
          /note="unnamed protein product;
          Catalytic activity: A. flavus omtB
          converts demethylsterigmatocystin
          (DMST) to sterigmatocystin (ST)
          and
          dihydrodemethylsterigmatocystin
          (DHDMST) to
          dihydrosterigmatocystin (DHST).
          Function: A. flavus omtB is a
          demethylsterigmatocystin
          6-O-methyltransferase involved in
          aflatoxin biosynthesis. Remark:
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          secondary metabolites. Title:
          strong similarity to
          O-methyltransferase omtB -
          Aspergillus flavus"
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          ADLVLTERVLRILAGIGYVAEHDVRVYIPTTMTR
          QMTDRLSGAVNDSFDIGMPTLAKV
          PEFLRMTNFGQNP SGAVKGALQYAEKTEM SLWDWV
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mRNA	join(<168480..169074, 169128..169245, 169293..169453, 169507..169540, 169597..>170002)	/locus-tag="An14g05850"
CDS	join(168480..169074, 169128..169245, 169293..169453, 169507..169540, 169597..170002)	/locus-tag="An14g05850"

/note="unnamed protein product;  
 Function: PTH11 of M. grisea is  
 required for appressorium  
 differentiation in response to  
 inductive surface cues. Function:  
 as do most fungal plant pathogens,  
 M. grisea differentiates an  
 infection structure specialized  
 for host penetration called the  
 appressorium. Phenotype: M. grisea  
 cells null mutant for PTH11 are no  
 more pathogenic. Similarity: the  
 similarity to PTH11 of M. grisea  
 is limited to the N-terminal half  
 of the predicted ORF. Title:  
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 protein PTH11 - Magnaporthe  
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/note="unnamed protein product;  
Function: PTH11 of *M. grisea* is  
required for appressorium  
differentiation in response to  
inductive surface cues. Function:  
as do most fungal plant pathogens,  
*M. grisea* differentiates an  
infection structure specialized  
for host penetration called the  
appressorium. Phenotype: *M. grisea*  
cells null mutant for PTH11 are no  
more pathogenic. Similarity: the  
length of the predicted ORF is  
only one half of the *M. grisea*  
PTH11. Title: similarity to  
integral membrane protein PTH11 -  
*Magnaporthe grisea*"

/citation=[63]

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CMQGRNTFYIVVGSIALAENFILVSMPLVVVWGM  
NLSPRQKVELSLIFGFGGLVCAIG  
LLRMVTFKRYVTADATTNGYLQAIWSIVELELGI  
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mRNA	join(<175066..175356, 175420..175941, 176025..176078, 176188..>176514)	/locus-tag="An14g05880"
CDS	join(175066..175356, 175420..175941, 176025..176078, 176188..176514)	/locus-tag="An14g05880"



		/inference="similar to AA sequence:UniProtKB:NCB9I2.2" /note="unnamed protein product; Similarity: the central part of the predicted ORF shows only weak similarity to N. crassa B9I2. 20. Title: strong similarity to hypothetical conserved protein B9I2.20 - Neurospora crassa" /codon-start=1 /protein-id="CAK42149.1" /db-xref="GI:134081894" /translation="MPLASDAFQADLSRLSPSHL EVSLPVTLSLAVLAYLLLVSTLRF QRVRILYRDYPQYTTTRASMSQMTVDDAWAIQKNI LQLEFPTTAVKALQFALFRTYGIP TISSLLLHTSQFSNPATSFKRYADTGALIGQFVT CPPTSSRARTAIARTKFLHSGYRA SGRILESDMLYTLSLFATEPIRFVERFEWRAMTE LERCAIGTYWKS LGDALDISYDEL PSGKSGFSDGLHFLEELRQWGDHYEENMRPDHR NRLVADKTMDVIVYGFPKWHILCD GFCKEPCADSLNQEVFSDTPNEDGRYYVQIWKGM PYYVQPTMWNRWGPAAWLTWALGL PLPGDDGDTYYPRGFDVADLGPRQFEGRGRKSVG EYVDVLEKEHKGQCPFGGRSDQPE ICLSR" /locus-tag="An14g05880" /number=1
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exon	175420..175941	/locus-tag="An14g05880" /number=2
intron	175942..176024	/locus-tag="An14g05880" /number=2
exon	176025..176078	/locus-tag="An14g05880" /number=3
intron	176079..176187	/locus-tag="An14g05880" /number=3
exon	176188..176514	/locus-tag="An14g05880" /number=4
gene	<176803..>178484	/locus-tag="An14g05890"
mRNA	join(<176803..177362, 177419..>178484)	/locus-tag="An14g05890"
CDS	join(176803..177362, 177419..178484)	/locus-tag="An14g05890"  /EC-number="5.2.-.-" /inference="profile:COGS:COG4716" /note="unnamed protein product; Remark: CLA compounds( cis,trans)-9,11-linoleic acid and (trans, cis)-10,12-linoleic acid are recognised nutritional supplements and effective inhibitors of epidermal carcinogenesis and forestomach neoplasia; furthermore CLA has also been shown to prevent adverse effects caused by immune stimulation in chicks, mice and rats, and has been shown to decrease the ratio of low density lipoprotein cholesterol to high

density lipoprotein cholesterol.  
 Remark: the linoleate isomerase is used in a method for producing conjugated linoleic/linolenic acid (CLA) from oils such as sunflower oil, safflower oil, corn oil, linseed oil, etc. Similarity: the N-terminal part of the prediction ORF shows also weak similarity to some oxidoreductases. Similarity: the patented protein, as well as the predicted ORF, show strong similarity to the 67 kDa myosin-crossreactive streptococcal antigen of Streptococcus pyogenes, a protein with unknown function, but involved in the pathogenesis of streptococcal infections.  
 Title: strong similarity to linoleate isomerase protein sequence PCA591 from patent WO9932604-A1 -Lactobacillus reuteri"

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 MPPFNDVCMEEELSLVPSKTNPNL  
 TVLEEFHEFWDEAVKDHPTFLTRHKHGLERI  
 DAKRASLGLRDRVDFMLASKSDK  
 SLGRSRICDHFNSFFKSYWMLLSTTFGIKPVH  
 SAAEFRRLQHYMHDIHEIHCRK  
 LDGGRYNRHESIVSPIAHFLCSRGVDVFRFHTTVT  
 DIITTPSSSEPHRVSAIKAIHENE  
 PEMTINLGERDIVLVSLGSMMSGSTTGNTSPPS  
 LELMDIEKDLDENWLLWLELSTKN  
 PIFGNAYNFCTRMAESRLESFTVTFSSPEFFNRF  
 TALTGDKVSGTFVTLKDTPWLLS  
 INLPQQPLFPDQPAHVQVLWGYAMPEREVDYIK  
 KPMLECSGQEIMEEILKQLNFPVQ  
 GILDHSITLPCVVPRAAATLLVRLRSDRPPVIPP  
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intron	177363..177418	/locus-tag="An14g05890" /number=1
exon	177419..178484	/locus-tag="An14g05890" /number=2
gene	complement(<179356..>181260)	/locus-tag="An14g05900"
mRNA	complement(join(<179356..179403, 179482..>181260))	/locus-tag="An14g05900"
CDS	complement(join(179356..179403, 179482..181260))	/locus-tag="An14g05900"

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/inference="similar to AA
sequence:PIR:T49456"
/note="unnamed protein product;
Similarity: other BLASTP hits are
explained by the relatively high
content of low-complexity regions.
Title: strong similarity to
hypothetical protein B14D6.80 -
Neurospora crassa"
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QLSIRRAHSHPPVVPASDSIFSDE
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KPPAWNGESDPIVFTSSAPEPTHNLPVRPAISSR
AVNTISLDDDDAGNSSDTRSNNRP
RKEAIQVSSDQLDFPDVDDLLDVAQRVEANAFSS
RTANLLATLEDRSRGSGESASRS
SRGRIQDQSDDIEVEEMPPPRKPQRKAIKVTSE
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ERKQKAKEDKAREKQLAADIAEVNKLKVDKKDST
HEMLIDLASTFTDTS LGNQTS ELM
RLKVDLSFFPSTIPNIVKWRKVRATYNDLSLGH
WEPCALHIRDEEEHVLC LIAAQDF
INMIVAPTTEPRNTINDHVERLKLAYPKSRPIYL
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PIHALVQP"

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03)

intron    complement(179404..1794 /locus-tag="An14g05900"
81)

exon      complement(179482..1812 /locus-tag="An14g05900"
60)

gene      complement(<181479..>18 /locus-tag="An14g05910"
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mRNA      complement(join(<181479 /locus-tag="An14g05910"
..182086,
182177..182601,
182623..>182990))

CDS       complement(join(181479. /locus-tag="An14g05910"
.182086,182177..182601,
182623..182990))

/EC-number="2.4.1.-"
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/inference="profile:PFAM:PF00534"
/inference="similar to AA
sequence:PIR:S64069"
/note="unnamed protein product;
Function: ALG2 of S. cerevisiae is
involved in N-glycosylation,
converting

```

man[2]glcnac-pp-dolichol to  
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 mannosyltransferase Alg2 -  
*Saccharomyces cerevisiae*"  
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 MAILRQLHLTWDLTCGETTSGDNG  
 EGEVEVFIVDQMPACVPFLKVRKQRILFYCHFPD  
 QLLARRDEGGSVLQLLKGLYRVPF  
 DWFEGWAVSASDKVVANSRFTRGVVSGVFGREKV  
 GDLSVVYPCVDTKAGDGEGGVVKD  
 GEKLWGGKKILLSVNRFERKKDLALAIRAYHGLG  
 EEKRKGTRLVVAGGYDNRVQENVQ  
 YHRELDELATGLGLQTATSKTVISALSIPDSIDV  
 LFLLSVPTAFRDLLLLQAKLLLYT  
 PINEHFGIVPVEAMRAGVPVLASNTGGPLETIVE  
 GETGWLRDAKVDADWTAVMDKVLV  
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intron	complement(182602..182622)	/locus-tag="An14g05910"
exon	complement(182623..182990)	/locus-tag="An14g05910"
gene	complement(<183872..>189440)	/locus-tag="An14g05920"
mRNA	complement(join(<183872..184411, 184472..188524, 188581..188756, 188813..189136, 189281..>189440))	/locus-tag="An14g05920"
CDS	complement(join(183872..184411,184472..188524, 188581..188756, 188813..189136, 189281..189440))	/locus-tag="An14g05920"

/inference="profile:COGS:COG5059"  
 /inference="profile:PFAM:PF00225"  
 /note="unnamed protein product;  
 Function: kinesins are  
 microtubule-dependent motor  
 proteins, involved in organelle

transport, in mitosis and meiosis, and in the transport of synaptic vesicles along axons of animal neurons. Similarity: the closest homologues, comprising XCENP-E of *X. laevis*, are involved in driving congression of chromosomes to the metaphase plate. Similarity: the main feature of the predicted ORF is to contain, in the N-terminal half, several kinesin-like domains, explaining the strong similarity to several different kinesin-like proteins. Similarity: the predicted ORF has just half of the length of XCENP-E of *X. laevis*; the best homologue, having also a corresponding length, is a *N. crassa* hypothetical protein. Title: strong similarity to kinesin-related protein XCENP-E - *Xenopus laevis*"

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RVFAETVDQDGVWDYLSDSVSSFLQGYNVSI  
LAY  
GQSGAGKSYTMGTSGPSEQSDPRS  
MGIIPRAAQLLEKLEGPAPKPNRNSGTGLRTPSR  
YSVGSASSFGKASVEKNWQLKATY  
VEIYNEQLRDLLVPESTHQGDRGTVTIREDAKGR  
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VMSPTPKDKRMSMPVDMMSGSDAS  
VMVDSKLHFVDLAGSERLKNTGASGERAKEG  
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YRDSKLTRLQLQDSLGGNAYTYMIACVNP  
AEFHLS  
ETVNTVQYAQRARAIQSKPRIQQI  
ADESDKHAVIERLKA EVAFLRQQLRNAEENG  
RRS  
AAPQDRAERQNEREVELQNQLLDT  
QESYNALSQRHAKLISEIARDSEHAGETDP  
NDV  
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VLEYEKTIQSLESSLNTRSSLSVTESTLL  
ERET  
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STETYLHELEARLDGQSTGEEKQA AIVAE  
LRKEL  
SRARESEANCEDYISTLEERLAEA  
DQDMELMQREMERLEHVIERQ RSLGKLDN  
LLYEL  
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DEGL  
TEPAPEAVHEASVEAEATAETDET  
NLKVLESATDRLEAQENGARASRASTPTQ  
TKVVA  
DKLETVTQELFDLRMQHESTVSEY  
EMLEAKYAEAMKALAEFQRDAAD EARP  
DEKVQD  
LLSTNVESRPVSFLEEGKAPGSND  
GKQPSSSPSLSSSEL SLAGEPASSHEQST  
LSNGEV  
PQENHVDTREIDEAKAQEVEQMRR  
LLMEHQEGVSIMSQKYAQLQSEHEGTL  
SLIETLK  
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KTSQSLIGTVDRAHRSLAALRNIAVEEFEARPDT  
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 LCAEEQERKISSLEGEVTELKSKH  
 HNAVESLOSSEQELSATLAELDKALASIDAMRSE  
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 SRVSELEKEIDSHKSLADSFKKDLESLQESHKQE  
 VTELEARATAAAQGDYESRFATMS  
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 DVTAEATMAEQIQEIMAQKHFSK  
 YAEMLDTNEDLRKQLETKGSDEGRL  
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 DQHHNRLSVIQQERDQALEDAKVK  
 IAAYEKDIETYRVRIEQLEIKNQDSSSHDRSSSIT  
 SNLRKSSSATSLSPPPAIPLPPL  
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 EARIRTIEKHLNAEKQLTATLEEA  
 LGDLEAQSNKVKSDCDAWKKKARELEEELTTLRK  
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gene	complement(<190148..>191691)	/locus-tag="An14g05930"
mRNA	complement(join(<190148..190283, 190763..190861, 190948..191206, 191652..>191691))	/locus-tag="An14g05930"
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191652..191691))

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192940..193251,
193625..193690,
193783..193884,
193959..>193985)) /locus-tag="An14g05940"
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193783..193884,
193959..193985))

/note="unnamed protein product;
Similarity: the similarity to NAB2
of M. musculus is weak, and the
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ORF is questionable. Title: weak
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protein 2 NAB2 - Mus musculus"
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SPAAFQSETSKNDKNGVPYPHVVGKGGTPDSVSV
PELQSIIRREPWNFFCRQYGNRSSP
PIASVYDLDPQIAIQGPSATIDSHQVGIMSVA
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PTWANAPAQPHPGSLQP"

/note="unnamed protein product;
Similarity: very weak similarity
to a fragment of protein SEQ ID
NO:917 of patent n. WO200042171-A1

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of *Eucalyptus grandis*. Title:  
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LQKFMQYLSQRRITFGRISLSPGS  
LAINEPLNPILWVMVLLIDRSVNRLGSRYSIIHF  
SVLDNKAGRLCCYDDIGIMRFYSW  
LQKCITSMEDLVYRIYIVGLVRNLHAMNVMCTLK  
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mRNA	complement(join(<194969..195817, 195865..196221, 196455..>196478))	/locus-tag="An14g05950"
CDS	complement(join(194969..195817,195865..196221,	/locus-tag="An14g05950"



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/note="Similarity: a short stretch
of amino acids of the predicted
ORF shows some weak similarity to
an A. thaliana hypothetical
protein."
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AERRVHYFEARTEKDGGWGIYRKGAVALTQPQRY
RDYPEIPDERIPSAIESFHCFLQA
LYLKPVVPYVGIGWRRMVLLGIRFQAVPRVREYI
EKIILPWTLTSTKPLLGLTDDILAY
TKMAQDIQCAQLYRECLIHLVGMAQYWGRNEFHN
AEHILTPSAYASLIRHVGTVQRQLI
EKADVALHTFIRTLATQKPRRIPNFLLRQFTDTV
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8879)
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197606..197698,
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198017..198238,
198288..198371,
198435..198525,
198598..198694,
198745..>198879))
CDS       complement(join(197258. /locus-tag="An14g05960"
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197606..197698,
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198435..198525,
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/EC-number="3.5.3.11"

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/inference="profile:COGS:COG0010"
/inference="profile:PFAM:PF00491"
/note="unnamed protein product;
Catalytic activity: H2O + agmatine
<=> urea + putrescine. Complex:
agmatinase of E. coli is a
homodimer of the speB gene
product. Function: agmatinase of
E. coli is part of the second
putrescine biosynthetic pathway;
it also represents the only
pathway for urea biosynthesis in
E. coli as no urease is present.
Similarity: the predicted ORF
shows much stronger similarity to
putative agmatinases of N. crassa
and S. pombe. Title: strong
similarity to agmatinase speB
-Escherichia coli"
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/citation=[10]
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YDNAWAIQQIEEGHNSVLMRKPFT
DAEKYGLSKAGKTLPRIITLGGDHTITLPLLRSI
NRAYGPVTVIHFDSHLDSWKPKVF
GGSPSQVAAINHGTYFYHAAMEGLLKNDTNIHAG
IRTTLSGPSDYENDGYCGFEIVEA
REIDTIGTDGIIKKIRERVGTENPVYLSIDIDTL
DPAYAPATGTPETGGWSTRELRTI
IRGLDGLNFIGADIVEVAPAYDTNAELSTMAAAD
VLYEVLTIMVKKGPLSVGRSDEL"
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79)
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197751..197968,
198017..198238,
198288..198371,
198435..198525,
198598..198694,
198745..198822))
exon complement(197258..1973 /product="unnamed"
42) /locus-tag="An14g05960"
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52) /locus-tag="An14g05960"
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gene	complement(<199830..>201412)	/locus-tag="An14g05970"
mRNA	complement(join(<199830..200758, 200827..>201412))	/locus-tag="An14g05970"
CDS	complement(join(199830..200758, 200827..201412))	
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		/inference="profile:PFAM:PF01554"
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		/note="unnamed protein product; Title: strong similarity to hypothetical protein SPAC11D3.06 - Schizosaccharomyces pombe"
		/codon-start=1
		/protein-id="CAK42158.1"
		/db-xref="GI:134081903"
		/translation="MYDSLPSYRETSSAHTHEE"

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TSPENLATTAFSLMFAMVTAWMIA  
LGGTTALDTLASSTFTGSSNKHDLGILLQRAFFV  
LGLFYVPVAILWTCSEPVFLLLGQ  
DPQLSRDSARFLTCLIPGGLGYIYFEAMKKYLQA  
QGIMRPGTYVLLITVPFNALLNYL  
FCYTFRMGLLGAPFATGISYWLSFALLVLYARFI  
AGSECWGGWSRKAFENLGT FARLA  
FLGVVHVGT EWFAFEIVALAAGRLGTIPLAAQSV  
IMTADQVLNTIPFGVG VATSSRVG  
SLLGSRDAAGASRAANTAAWLSMALGGAVLAVLM  
GTRHVF AKIFNSDEGVVQLTAEVL  
PWVALFQIADGLNGSCGSLRGMGRQHVGALVNL  
ASY YCGALPLGIWLA FN GWGLKGL  
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exon	complement(200827..201412)	/locus-tag="An14g05970"
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mRNA	join(<202677..203229, 203273..203374, 203431..>204146)	/locus-tag="An14g05980"
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/inference="similar to AA  
sequence:PIR:S61140"  
/note="unnamed protein product;  
Function: TPO3 of S. cerevisiae is a vacuolar polyamine transporter, that controls the cytoplasmic spermine content. Phenotype: S. cerevisiae cells in which TPO3 was disrupted showed an increased sensitivity to polyamine toxicity and a decrease in polyamine uptake activity and polyamine content in vacuoles. Phenotype: S. cerevisiae cells overexpressing TPO3 were resistant to polyamine toxicity and showed an increase in polyamine uptake activity and polyamine content in vacuoles.  
Remark: TPO3 of S. cerevisiae is also called YPR156c or P9584. 7.  
Similarity: the predicted ORF is 125 amino acids longer at the N-terminus than TPO3 of S. cerevisiae. Title: strong similarity to polyamine transport protein Tpo3 - Saccharomyces cerevisiae"  
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		<pre> /protein-id="CAK42159.1" /db-xref="GI:134081904" /translation="MNLKLTQIDLVPVPEKQSAS DIDSLPVEQHGTHTHPAPTS DPLD PLNWPRWRKHVILGIVMLKFVLPEQSRRLHRLTM NRYFLFTYITTTTVPSFAEIQSQY DINYSQVNWTVAIPALGLSLGPLFWSSVGDYGR RIVFIVGTVIALVATIGA AAVADTY GGYMAARFFQGFVSPSSTVGMAVANGTVTDMFY EYERGQKLGLWVLALDSGLLLGPT FGGFLNLVSAQWINWFNAILFAALLLLELTLMPE TLYPRALMLQRMVTEKPAESNAG IEEAGIKRTKSLPFFNLRPIPGLSHPPIYASLTR FLLTFRFPVIAVAVIGYSFTWYWW ILSVITMVPSAYATDSPLIQGLLFLGLLIGTLVA EVSCSGRLSDAIVGRLAKRNGGVR VPEMRLWLAYPAIVLTAGVYIPIAHVRTISNIAI QPAVGLILWGISIDKAYHWMVGQV AFFLCE" </pre>
exon	202677..203229	<pre> /locus-tag="An14g05980" /number=1 </pre>
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intron	203375..203430	<pre> /locus-tag="An14g05980" /number=2 </pre>
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gene	complement(<205094..>207843)	<pre> /locus-tag="An14g05990" </pre>
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CDS	complement(join(205094..207273,207361..207431, 207517..207554, 207700..207843))	<pre> /locus-tag="An14g05990"  /note="unnamed protein product; Title: weak similarity to spindle pole body-associated protein sadlp - Schizosaccharomyces pombe" /codon-start=1 /protein-id="CAK42160.1" /db-xref="GI:134081905" /translation="MRNLVYPKYHVLESLNRPCD AVDRHSTRVFSRRVAFALEGRQLP RIAIDTSELVILVAAIVALASPALDLCRLQASY SVPSSHTNRNIKPILLRIELPMPA RRGATRRAGSTRSDIGSASTYFQSKLGPEARTQA LPNLPTKQSFAYGSAETPILPREL KIQPHMDLTEMADAIDKGIEDAKDRQMKEKETQ DKSRRQKSPSITRSPVRRSRREPT PDELQLLDNLREATKSPTPVRGNYSNNDQSTATP TPPIPHTLSTASSPAQSLPVPRYP HVPAENLYSPMGRFGPQLHDGPPLGSSPLPDDS SLYSFTVERAINSDELTRTLSDGK NIKAPPRRFSGLAFANEPHHEEEEPDSRLLKTKS RSPSLQPSYEDFQIEPSPEPEPQS EPESVQELELEPTPEPEPIPELEPMPEPTPEPEV IREKSPAAQFTAPTCTLIPNAYAR </pre>

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RSSPTPIMPSPRGSTD LGPPT EQKTNFLSIGLGV
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LWRGSHYRPASPPLAALVPWEDYGDCWCSTPRDG
MSQIGIDLGQKIVPEEVAVEHMPK
TATLKPENAPREMELWAQYVLVQKTSRPARTQA
ERFSIHKPIMDALRSAWPTEDPTA
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exon      complement(207361..2074 /locus-tag="An14g05990"
31)
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16)
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54)
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mRNA      complement(join(<208451 /locus-tag="An14g06000"
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CDS       complement(join(208451. /locus-tag="An14g06000"
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209889..210489,
210572..210658))

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/note="unnamed protein product;
Function: MDV1 of S. cerevisiae is
involved in the mitochondrial
membrane fission event by
regulating the assembly of Dnm1p,
a dynamin-related GTPase, into
punctate structures at the outer
mitochondrial membrane. Phenotype:
the mitochondrial fission is
blocked in S. cerevisiae MDV null

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mutants and mitochondrial membranes form nets. Remark: is also called YJL112w, NET2, FIS2 or GAG3. Title: strong similarity to mitochondrial fission protein Mdv1 - *Saccharomyces cerevisiae*"  
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SRAISSLPDELLANIPDDSSSYSLFQGFQASQDD  
IEYRRARRRRSSSKSKLLKDGETR  
GALPSAPSDLKKERDLLSRMELMGVRKNMCSSE  
IHDIDNKIANLHNMRKIVLDRLAG  
LEMEEADLEHELNEIENKLEDIQEEQQEAEVPPP  
ATPKSSEANDDSIVSEDPAMGASF  
MSESIYQKIPSPKSVKQRSIILHEHFAPGSEIKE  
MPAHSMDMVT AIDFDYFPGTMISAA  
LDDTVRVWDLNVGRCVGFLEGHNASVRCLQIEDN  
IVATGSM DASVKLWDL SRARTTTR  
DNRVTRREDDEESAQADDASMASHSTTLED CYVY  
SLDAHVDEV TALHFKGDTLISGSA  
DKTLRQWDLVKGRCVQTL DVLWAAAQASTLGSET  
TWRPSGRLPDASAD FVGAVQCFDA  
ALACGTADGMVRLWDLRSGQVHRSLVGHTGPITC  
LQFDDVHLVTGSQDRSIRI WDLRT  
GSIFDAYAYDKPITSMMFDTKRIVAAAGENVVKV  
YDKADGHHWDCGAGVGVD DSGPQP  
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mRNA	join(<211445..211515, 211743..212394, 212451..>212528)	/locus-tag="An14g06010"
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exon	211445..211515	/locus-tag="An14g06010"
intron	211516..211742	/number=1 /locus-tag="An14g06010"
exon	211743..212394	/number=1 /locus-tag="An14g06010"
intron	212395..212450	/number=2 /locus-tag="An14g06010"
exon	212451..212528	/number=2 /locus-tag="An14g06010"
gene	complement(<212729..>21 3754)	/number=3 /locus-tag="An14g06020"
mRNA	complement(join(<212729 ..213283, 213342..213578, 213671..>213754))	/locus-tag="An14g06020"
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intron	complement(213284..213341)	/number=1 /locus-tag="An14g06020"
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intron	complement(213579..213670)	/number=2 /locus-tag="An14g06020"
exon	complement(213671..213754)	/number=2 /locus-tag="An14g06020"
gene	<214408..>214606	/number=3 /locus-tag="An14g06030"
mRNA	join(<214408..214444, 214506..>214606)	/locus-tag="An14g06030"
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exon	214506..214606	/number=1 /locus-tag="An14g06030"
gene	complement(<216128..>217084)	/number=2 /locus-tag="An14g06040"
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exon	217593..217931	/locus-tag="An14g06050"
intron	217932..218002	/number=1 /locus-tag="An14g06050"
exon	218003..218104	/number=1 /locus-tag="An14g06050"
gene	complement(<218542..>219708)	/number=2 /locus-tag="An14g06060"
mRNA	complement(<218542..>219708)	/locus-tag="An14g06060"
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/inference="similar to AA  
 sequence:UniProtKB:SC05211.1"  
 /note="unnamed protein product;  
 Function: TTP1 of *S. cerevisiae* is  
 involved in the transfer of  
 mannose residues to the mannans of  
 glycoproteins during maturation in  
 the Golgi. Function: the correct  
 mannosylation of proteins by TTP1  
 of *S. cerevisiae* is essential for  
 growth and morphogenesis. Golgi  
 Phenotype: the N-linked sugar  
 residues in the *S. cerevisiae* TTP1  
 null mutant lack the main  
 alpha-1,2-linked branches of the  
 mannan. Remark: TTP1 of *S.*  
*cerevisiae* is also called *mn2* or  
*YBR015C*. Title: strong similarity  
 to alpha-1,2-mannosyltransferase  
 Ttp1 - *Saccharomyces cerevisiae*"  
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 FAVLFSSFEVVIWMDADCFPLHKPEVLLESEPF  
 SKGLVTWPDFWISSASPLYFTISR  
 QEMPALSERASSEAGVFLVSKKTHQMTLLLAAYY  
 NYYGPSHYFRLLSQGAPGEGDKET  
 FLHAASAVGEPFYAVSERVQAVGHTKPGGIAGSA  
 MVQTDPAEDYALTSAGKWRVQDES  
 VAKAPRAFFIHANYPKFNPGEKVFGMKWETTPTL  
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exon	complement(218542..219708)	/locus-tag="An14g06060"
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gene	<221804..>226148	/locus-tag="An14g06070"
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CDS	join(221804..221887, 221930..224173, 224489..224622, 224729..224737, 224926..224987, 225102..225280, 225490..225530,	/locus-tag="An14g06070"

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225858..225905,  
225959..225993,  
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crassa"  
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RRLCSPEYYTVDSHVKPNHHNPYS  
SRATKTDSLKQYHAPLVANPDSSRAWMGLEQTPV  
PIQCPWPALTPEQKDNASDEQHEE  
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RTYILRLAQESTSLQEAIATLASCNLRQRRERG  
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TGSECVRADHRAIIRQCKDLSD  
SGFFNNLSCLQLLEKIWAENPAVDVIPVVSSLDF  
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GIATGGLNITIYIRFRPHHRIDG  
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221761	tctgcaccct	agcagttggc	caacctctgc	gtcggatccg	gctatggaac	caacctcgaa
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222121	tccacgagca	gtgtccaaat	cgcaaccggc	tcttgacaca	gccgcagaaa	aacgacgact
222181	tcatgataag	cagcgttcat	cagccgcggg	gcttacagag	catgggtctg	tctcgattcc
222241	acctacttca	caacgcgcgt	tgtgctcacc	ggagtactac	actgtggatt	cccatgttaa
222301	gccgaatcac	cataatcctt	attcttcacg	tgcgacaaag	accgattctt	tgaacaata
222361	ccatgccccca	ttggtcgcaa	accccgattc	atcaagggcc	tggatggggg	tagaacagac
222421	accggtaccg	atacagtgtc	cgtggccagc	cctgactccg	gaacagaaaag	ataatgcttc
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223561	acctctcttt	acatccagcc	acgcctacat	ctcgccacct	tcatcgccga	cagaccagcc
223621	ggtggtcgca	gctcacaatc	tcaaggacgt	catacacatc	tctgagtcac	tccgtcatgc
223681	ggcgatcttg	tacgcgagc	gactgccta	tccagacctc	ccgtccgac	acctcgtat
223741	tcaaaacatt	gtgcaacaca	taatgagtca	cattatgacc	gttcaatctg	acgcgtatct
223801	cctgtggcca	ctattcatca	ccgggtcgga	gtgcgtgcgt	gccgatcatc	gcgccattat
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223921	gcagctcctg	gagaagatct	gggcagagaa	ccctgccgtg	gatgtgatcc	ctgttgtctc
223981	atcccttgat	ttcggcttgc	aggcagccgc	cagcgggtgc	gtgagcgagg	ttacatttct
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224101	tgtctctcgg	aagcagggat	tccgctggca	cgaggcgatg	caaaccaaa	gcgcggagga
224161	cgagtatatg	actgtatgac	gtgacctgac	ggatacgtgc	atcaaaacga	cgagtccagc
224221	atgaattgcg	aggaccaatt	ataatataga	ggtatcatat	tagcgaaata	taatgaacat
224281	aatgcaacat	tccccacta	cgtacacagt	actgtgtgcc	ctcagtatct	gtctatggca
224341	acctgaacct	tcggggccaca	acaggccccc	actatcgga	ccatcgcact	agatccgttc
224401	ccacttccca	cacaatccgc	tcgatacgtc	ccatcacgac	agtaccctac	tgcgtaaaat
224461	tctccgtaaa	cctactgtca	tctgtcagaa	ctccatcgat	gatgcattca	ctccatctgg
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224581	gcatctccc	agcgccagta	cgtcggaaaa	tttgtgttgg	aggtgagttg	agtttcgggt
224641	ctgcgtgtca	gatgctcatt	tgtgggtgtt	ggactctgag	aggggtgtcca	cccatcactt
224701	agatagtact	gtgccgctgt	ggtgatagaa	tgagtgggta	agtaattgcc	taactcttgg
224761	agagaagggg	tcttgtttcac	tttgtttctt	gaattactgg	tttgggtatg	cggagggggg
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224881	gtagttagta	tgtagttaag	gcacagtagt	ataccactat	tatagtaata	gtagtggcag
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 226501 tta

L5 ANSWER 26 OF 27 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): AE014133 GenBank (R)  
 GenBank ACC. NO. (GBN): AE014133 AE014853-AE015037  
 GenBank VERSION (VER): AE014133.1 GI:24378526  
 SEQUENCE LENGTH (SQL): 2030921  
 MOLECULE TYPE (CI): DNA; circular  
 DIVISION CODE (CI): Bacteria  
 DATE (DATE): 24 Jan 2006  
 DEFINITION (DEF): Streptococcus mutans UA159, complete genome.  
 SOURCE: Streptococcus mutans UA159  
 ORGANISM (ORGN): Streptococcus mutans UA159  
 Bacteria; Firmicutes; Lactobacillales;  
 Streptococcaceae; Streptococcus

COMMENT:

On or before Jan 18, 2006 this sequence version replaced  
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REFERENCE: 1 (bases 1 to 2030921)  
 AUTHOR (AU): Ajdic,D.; McShan,W.M.; McLaughlin,R.E.; Savic,G.;  
 Chang,J.; Carson,M.B.; Primeaux,C.; Tian,R.; Kenton,S.;  
 Jia,H.; Lin,S.; Qian,Y.; Li,S.; Zhu,H.; Najjar,F.;  
 Lai,H.; White,J.; Roe,B.A.; Ferretti,J.J.  
 TITLE (TI): Genome sequence of Streptococcus mutans UA159, a  
 cariogenic dental pathogen  
 JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 99 (22), 14434-14439  
 (2002)  
 OTHER SOURCE (OS): CA 137:364100  
 REFERENCE: 2 (bases 1 to 2030921)  
 AUTHOR (AU): Ajdic,D.; McShan,W.M.; McLaughlin,R.E.; Savic,G.;  
 Chang,J.; Carson,M.B.; Primeaux,C.; Tian,R.; Kenton,S.;  
 Jia,H.; Lin,S.; Qian,Y.; Li,S.; Zhu,H.; Najjar,F.;  
 Lai,H.; White,J.; Roe,B.A.; Ferretti,J.J.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (09-JUL-2002) Department of Microbiology and  
 Immunology, University of Oklahoma Health Sciences  
 Center, 940 SL Young Blvd., Oklahoma City, OK 73104,  
 USA

FEATURES (FEAT):  

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source	1..2030921	/organism="Streptococcus mutans UA159" /mol-type="genomic DNA" /strain="UA159" /db-xref="taxon:210007"

L5 ANSWER 27 OF 27 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): BX571856 GenBank (R)  
 GenBank ACC. NO. (GBN): BX571856  
 GenBank VERSION (VER): BX571856.1 GI:49240382  
 CAS REGISTRY NO. (RN): 726687-34-9  
 SEQUENCE LENGTH (SQL): 2902619  
 MOLECULE TYPE (CI): DNA; circular  
 DIVISION CODE (CI): Bacteria  
 DATE (DATE): 7 Oct 2006  
 DEFINITION (DEF): Staphylococcus aureus subsp. aureus strain MRSA252,  
 complete genome.  
 KEYWORDS (ST): complete genome  
 SOURCE: Staphylococcus aureus subsp. aureus MRSA252  
 ORGANISM (ORGN): Staphylococcus aureus subsp. aureus MRSA252

REFERENCE: Bacteria; Firmicutes; Bacillales; Staphylococcus  
 1 (bases 1 to 2902619)  
 AUTHOR (AU): Holden,M.T.; Feil,E.J.; Lindsay,J.A.; Peacock,S.J.;  
 Day,N.P.; Enright,M.C.; Foster,T.J.; Moore,C.E.;  
 Hurst,L.; Atkin,R.; Barron,A.; Bason,N.; Bentley,S.D.;  
 Chillingworth,C.; Chillingworth,T.; Churcher,C.;  
 Clark,L.; Corton,C.; Cronin,A.; Doggett,J.; Dowd,L.;  
 Feltwell,T.; Hance,Z.; Harris,B.; Hauser,H.;  
 Holroyd,S.; Jagels,K.; James,K.D.; Lennard,N.; Line,A.;  
 Mayes,R.; Moule,S.; Mungall,K.; Ormond,D.; Quail,M.A.;  
 Rabbino-witsch,E.; Rutherford,K.; Sanders,M.; Sharp,S.;  
 Simmonds,M.; Stevens,K.; Whitehead,S.; Barrell,B.G.;  
 Spratt,B.G.; Parkhill,J.  
 TITLE (TI): Complete genomes of two clinical Staphylococcus aureus  
 strains: evidence for the rapid evolution of virulence  
 and drug resistance  
 JOURNAL (SO): Proc. Natl. Acad. Sci. U.S.A., 101 (26), 9786-9791  
 (2004)  
 OTHER SOURCE (OS): CA 141:152000  
 REFERENCE: 2 (bases 1 to 2902619)  
 AUTHOR (AU): Holden,M.T.G.  
 TITLE (TI): Direct Submission  
 JOURNAL (SO): Submitted (23-JUN-2004) Submitted on behalf of the  
 Pathogen Sequencing Unit, Sanger Institute, Wellcome  
 Trust Genome Campus, Hinxton, Cambridge CB10 1SA,  
 E-mail: mh3@sanger.ac.uk

FEATURES (FEAT):

Feature Key	Location	Qualifier
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=> d 15 20

L5 ANSWER 20 OF 27 USPATFULL on STN  
 AN 2003:71519 USPATFULL  
 TI Corynebacterium glutamicum genes encoding metabolic pathway proteins  
 IN Pompejus, Markus, Freinsheim, GERMANY, FEDERAL REPUBLIC OF  
 Kroger, Burkhard, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF  
 Schroder, Hartwig, Nussloch, GERMANY, FEDERAL REPUBLIC OF  
 Zelder, Oskar, Speyer, GERMANY, FEDERAL REPUBLIC OF  
 Haberhauer, Gregor, Limburgerhof, GERMANY, FEDERAL REPUBLIC OF  
 Kim, Jun-Won, Seoul, KOREA, REPUBLIC OF  
 Lee, Heung-Shick, Seoul, KOREA, REPUBLIC OF  
 Hwang, Byung-Joon, Seoul, KOREA, REPUBLIC OF  
 PI US 20030049804 A1 20030313  
 AI US 2000-746660 A1 20001222 (9)  
 RLI Continuation-in-part of Ser. No. US 2000-606740, filed on 23 Jun 2000,  
 PENDING Continuation-in-part of Ser. No. US 2000-603124, filed on 23 Jun  
 2000, PENDING  
 PRAI DE 1999-19931420 19990708  
 US 1999-141031P 19990625 (60)  
 US 1999-142101P 19990702 (60)  
 US 1999-148613P 19990812 (60)  
 US 2000-187970P 20000309 (60)

DT Utility  
FS APPLICATION  
LN.CNT 15004  
INCL INCLM: 435/115.000  
INCLS: 435/069.100; 435/252.300; 435/320.100; 435/183.000; 536/023.200  
NCL NCLM: 435/115.000  
NCLS: 435/069.100; 435/183.000; 435/252.300; 435/320.100; 536/023.200  
IC [7]  
ICM C12P013-08  
ICS C07H021-04; C12N009-00; C12P021-02; C12N001-21  
IPCI C12P0013-08 [ICM,7]; C12P0013-00 [ICM,7,C\*]; C07H0021-04 [ICS,7];  
C07H0021-00 [ICS,7,C\*]; C12N0009-00 [ICS,7]; C12P0021-02 [ICS,7];  
C12N0001-21 [ICS,7]  
IPCR C07K0014-195 [I,C\*]; C07K0014-34 [I,A]; C12N0001-21 [I,C\*];  
C12N0001-21 [I,A]; C12N0009-00 [I,C\*]; C12N0009-00 [I,A];  
C12N0009-18 [I,C\*]; C12N0009-18 [I,A]; C12N0009-90 [I,C\*];  
C12N0009-90 [I,A]  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 21

L5 ANSWER 21 OF 27 USPATFULL on STN  
AN 2003:95966 USPATFULL  
TI Polynucleotides, materials incorporating them, and methods for using  
them  
IN Glenn, Matthew, Auckland, NEW ZEALAND  
Havukkala, Ilkka J., Auckland, NEW ZEALAND  
Bloksberg, Leonard N., Auckland, NEW ZEALAND  
Lubbers, Mark W., Palmerston North, NEW ZEALAND  
Dekker, James, Palmerston North, NEW ZEALAND  
Christensson, Anna C., Lund, SWEDEN  
Holland, Ross, Palmerston North, NEW ZEALAND  
O'Toole, Paul W., Palmerston North, NEW ZEALAND  
Reid, Julian R., Palmerston North, NEW ZEALAND  
Coolbear, Timothy, Palmerston North, NEW ZEALAND  
PA Genesis Research & Development Corp. Ltd, Parnell, NEW ZEALAND (non-U.S.  
corporation)  
Via Lachia Bioscience (NZ) Ltd., Auckland, NEW ZEALAND (non-U.S.  
corporation)  
PI US 6544772 B1 20030408  
AI US 2000-634238 20000808 (9)  
DT Utility  
FS GRANTED  
LN.CNT 2015  
INCL INCLM: 435/252.300  
INCLS: 435/320.100; 536/023.700  
NCL NCLM: 435/252.300  
NCLS: 435/320.100; 536/023.700  
IC [7]  
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ICS C12N015-63; C12N015-31  
IPCI C12N0001-21 [ICM,7]; C12N0015-63 [ICS,7]; C12N0015-31 [ICS,7]  
IPCR A23C0019-00 [I,C\*]; A23C0019-032 [I,A]; C07K0014-195 [I,C\*];  
C07K0014-335 [I,A]; C12N0001-21 [I,C\*]; C12N0001-21 [I,A];  
C12N0015-31 [I,C\*]; C12N0015-31 [I,A]  
EXF 435/252.3; 435/320.1; 536/23.7  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d 15 22

L5 ANSWER 22 OF 27 BIOTECHDS COPYRIGHT 2008 THOMSON REUTERS on STN  
 AN 1999-00562 BIOTECHDS  
 TI Use of lactic and propionic acid bacteria;  
 to bind mycotoxin to prevent their absorption or to purify  
 contaminated food or feedstuff  
 AU El-Nezami H; Kankaanpaa P; Salminen S; Ahokas J  
 PA Roy.Melbourne-Inst.Technol.  
 LO Melbourne, Victoria, Australia.  
 PI WO 9834503 13 Aug 1998  
 AI WO 1998-AU63 6 Feb 1998  
 PRAI AU 1997-5005 7 Feb 1997  
 DT Patent  
 LA English  
 OS WPI: 1998-557001 [49]

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 CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,  
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 SEA LACTOBACILLUS REUTERI AND TOXIN(P)BIND? AND CD4+ CELLS  
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 SEA LACTOBACILLUS REUTERI AND TOXIN(P)BIND?  
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0\* FILE ADISNEWS  
 0\* FILE ANTE  
 0\* FILE AQUALINE  
 0\* FILE BIOENG  
 1\* FILE BIOTECHABS  
 1\* FILE BIOTECHDS  
 0\* FILE BIOTECHNO  
 2 FILE CAPLUS  
 0\* FILE CEABA-VTB  
 0\* FILE CIN  
 0\* FILE ESBIODBASE  
 0\* FILE FOMAD  
 0\* FILE FOREGE  
 2\* FILE FROSTI  
 0\* FILE FSTA  
 5 FILE GENBANK  
 1 FILE IFIPAT  
 0\* FILE KOSMET  
 0\* FILE NTIS  
 0\* FILE NUTRACEUT  
 1\* FILE PASCAL  
 0\* FILE PHARMAML  
 1 FILE SCISEARCH  
 1 FILE TOXCENTER  
 21 FILE USPATFULL  
 3 FILE USPAT2  
 0\* FILE WATER  
 2 FILE WPIDS  
 2 FILE WPINDEX

L1 QUE LACTOBACILLUS REUTERI AND TOXIN(P) BIND?

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FILE 'BIOTECHDS, CAPLUS, FROSTI, GENBANK, IFIPAT, PASCAL, SCISEARCH,  
TOXCENTER, USPATFULL, USPAT2' ENTERED AT 13:59:37 ON 07 JUL 2008

L2 38 S L1  
L3 34 DUP REM L2 (4 DUPLICATES REMOVED)  
L4 27 S L3 AND (TABLET OR FOOD OR DIETARY SUPPLEMENT OR CONFECTIONERY  
L5 27 DUP REM L4 (0 DUPLICATES REMOVED)

=> logoff

ALL L# QUERIES AND ANSWER SETS ARE DELETED AT LOGOFF

LOGOFF? (Y)/N/HOLD:y

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

FULL ESTIMATED COST

174.83

178.94

STN INTERNATIONAL LOGOFF AT 14:06:30 ON 07 JUL 2008

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:ssspt189dxw

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

\* \* \* \* \* Welcome to STN International \* \* \* \* \*

NEWS 1 Web Page for STN Seminar Schedule - N. America  
NEWS 2 NOV 21 CAS patent coverage to include exemplified prophetic  
substances identified in English-, French-, German-,  
and Japanese-language basic patents from 2004-present  
NEWS 3 NOV 26 MARPAT enhanced with FSORT command  
NEWS 4 NOV 26 CHEMSAFE now available on STN Easy  
NEWS 5 NOV 26 Two new SET commands increase convenience of STN  
searching  
NEWS 6 DEC 01 ChemPort single article sales feature unavailable  
NEWS 7 DEC 12 GBFULL now offers single source for full-text  
coverage of complete UK patent families  
NEWS 8 DEC 17 Fifty-one pharmaceutical ingredients added to PS  
NEWS 9 JAN 06 The retention policy for unread STNmail messages  
will change in 2009 for STN-Columbus and STN-Tokyo  
NEWS 10 JAN 07 WPIDS, WPINDEX, and WPIX enhanced Japanese Patent  
Classification Data  
NEWS 11 FEB 02 Simultaneous left and right truncation (SLART) added  
for CERAB, COMPUAB, ELCOM, and SOLIDSTATE  
NEWS 12 FEB 02 GENBANK enhanced with SET PLURALS and SET SPELLING  
NEWS 13 FEB 06 Patent sequence location (PSL) data added to USGENE  
NEWS 14 FEB 10 COMPENDEX reloaded and enhanced  
NEWS 15 FEB 11 WTEXTILES reloaded and enhanced  
NEWS 16 FEB 19 New patent-examiner citations in 300,000 CA/Caplus  
patent records provide insights into related prior  
art  
NEWS 17 FEB 19 Increase the precision of your patent queries -- use  
terms from the IPC Thesaurus, Version 2009.01

NEWS 18 FEB 23 Several formats for image display and print options discontinued in USPATFULL and USPAT2

NEWS 19 FEB 23 MEDLINE now offers more precise author group fields and 2009 MeSH terms

NEWS 20 FEB 23 TOXCENTER updates mirror those of MEDLINE - more precise author group fields and 2009 MeSH terms

NEWS 21 FEB 23 Three million new patent records blast AEROSPACE into STN patent clusters

NEWS 22 FEB 25 USGENE enhanced with patent family and legal status display data from INPADOCDB

NEWS 23 MAR 06 INPADOCDB and INPAFAMDB enhanced with new display formats

NEWS 24 MAR 11 EPFULL backfile enhanced with additional full-text applications and grants

NEWS 25 MAR 11 ESBIOBASE reloaded and enhanced

NEWS 26 MAR 20 CAS databases on STN enhanced with new super role for nanomaterial substances

NEWS 27 MAR 23 CA/CAPLUS enhanced with more than 250,000 patent equivalents from China

NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,  
AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.

NEWS HOURS STN Operating Hours Plus Help Desk Availability

NEWS LOGIN Welcome Banner and News Items

NEWS IPC8 For general information regarding STN implementation of IPC 8

Enter NEWS followed by the item number or name to see news on that specific topic.

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\* \* \* \* \* STN Columbus \* \* \* \* \*

FILE 'HOME' ENTERED AT 17:02:18 ON 29 MAR 2009

=> index bioscience

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED

COST IN U.S. DOLLARS

SINCE FILE TOTAL

ENTRY SESSION

FULL ESTIMATED COST

0.22 0.22

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE, AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS, CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB, DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 17:02:31 ON 29 MAR 2009

68 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view search error messages that display as 0\* with SET DETAIL OFF.

=> s Lactobacillus reuteri and toxi? and CD+4(p)lymphocyte? and cultur?

0\* FILE ADISNEWS

0\* FILE ANTE

0\* FILE AQUALINE

0\* FILE BIOENG



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0* FILE BIOTECHABS
0* FILE BIOTECHDS
0* FILE BIOTECHNO
0* FILE CEABA-VTB
0* FILE CIN
21 FILES SEARCHED...
0* FILE FOMAD
0* FILE FOREGE
0* FILE FROSTI
0* FILE FSTA
0* FILE KOSMET
43 FILES SEARCHED...
0* FILE NTIS
0* FILE NUTRACEUT
0* FILE PASCAL
0* FILE PHARMAML
61 FILES SEARCHED...
0* FILE WATER

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0 FILES HAVE ONE OR MORE ANSWERS, 68 FILES SEARCHED IN STNINDEX

L1 QUE LACTOBACILLUS REUTERI AND TOXI? AND CD+4(P) LYMPHOCYTE? AND CULTUR?

=> logoff

ALL L# QUERIES AND ANSWER SETS ARE DELETED AT LOGOFF

LOGOFF? (Y)/N/HOLD:y

COST IN U.S. DOLLARS

FULL ESTIMATED COST

SINCE FILE	TOTAL
ENTRY	SESSION
2.04	2.26

STN INTERNATIONAL LOGOFF AT 17:04:21 ON 29 MAR 2009